

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2000, 16:43:29 ; Search time 2244.69 Seconds
(without alignments)
3897.314 Million cell updates/sec

Title: us-09-236-468a-1
Perfect score: 2003
Sequence: 1 gtttctctggcagcagcaag.....atttctctgtgattgttca 2003

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_om.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl1.*
- 8: gb_pl2.*
- 9: gb_pr1.*
- 10: gb_pr2.*
- 11: gb_pr3.*
- 12: gb_ro.*
- 13: gb_sy.*
- 14: gb_un.*
- 15: em_fun.*
- 16: em_hum1.*
- 17: em_hum2.*
- 18: em_in.*
- 19: em_om.*
- 20: em_or.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
- 24: em_pl.*
- 25: em_ro.*
- 26: em_sts.*
- 27: em_sy.*
- 28: em_un.*
- 29: em_vi.*
- 30: gb_htg1.*
- 31: gb_htg2.*
- 32: gb_in1.*
- 33: gb_in2.*
- 34: em_ba1.*
- 35: em_ba2.*
- 36: em_hum3.*
- 37: em_hum4.*
- 38: gb_pr4.*
- 39: gb_htg3.*
- 40: gb_htg4.*
- 41: gb_htg5.*
- 42: gb_htg6.*
- 43: gb_htg7.*

- 44: em_htg1.*
- 45: em_htg2.*
- 46: em_htg3.*
- 47: em_hum5.*
- 48: gb_pl3.*
- 49: gb_pr5.*
- 50: gb_htg8.*
- 51: gb_htg9.*
- 52: gb_htg10.*
- 53: gb_htg11.*
- 54: gb_htg12.*
- 55: gb_htg13.*
- 56: gb_htg14.*
- 57: gb_in3.*
- 58: gb_htg15.*
- 59: gb_htg16.*
- 60: gb_htg17.*
- 61: em_htg4.*
- 62: em_htg5.*
- 63: em_htg6.*
- 64: em_htg7.*
- 65: em_hum6.*
- 66: gb_htg18.*
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- 69: gb_htg21.*
- 70: gb_htg22.*
- 71: gb_htg23.*
- 72: gb_vl1.*
- 73: gb_vl2.*
- 74: gb_ba3.*
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- 87: em_htg20.*
- 88: em_htg21.*
- 89: em_htg22.*
- 90: em_htg23.*
- 91: gb_pr6.*
- 92: gb_pr7.*
- 93: gb_sts1.*
- 94: gb_sts2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1942.2	97.0	2641	91	HSU25128
2	1942.2	97.0	2641	93	G26909
3	1156.6	57.7	1977	12	RNU55836
4	620	31.0	1980	91	HSETHR05
5	620	31.0	159700	39	AC010822
6	620	31.0	173316	43	AC019185
7	594.4	29.7	2429	4	AF132082
8	486.4	24.3	2129	4	AF132084
9	452.6	22.6	1862	5	I17764
10	452.6	22.6	1863	5	I17765
11	452.6	22.6	1878	3	OPOPTH
12	445.2	22.2	1836	12	RATPTH

13	445.2	22.2	2051	5	IL17766	IL17766 Sequence 3
14	445.2	22.2	2065	12	RMPHPR	M7184 Rat parathy
15	437.2	21.8	1984	12	MMHPRR	X78936 M.musculus
16	435.6	21.7	2177	3	AF167095	AF167095 Canis fam
17	432	21.6	1948	92	HUMPHRR	L04308 Human parat
18	430.8	21.5	2067	3	SSU18315	U18315 Sus scrofa
19	430.4	21.5	2010	5	IL17767	IL17767 Sequence 4
20	430.4	21.5	2095	91	HSPHR	X68596 H.sapiens m
21	430.4	21.5	2171	91	HSU17418	U17418 Human parat
22	415.6	20.7	2152	4	AF132085	AF132085 Danio rer
23	402.8	20.1	507	12	AF132083	AF132083 Mus muscu
24	197	9.8	234812	40	AC012362	AC012362 Homo sapi
25	189.6	9.5	381	4	MGU94326	U94326 Meleagris g
26	176	8.8	1987	4	AF100644	AF100644 Rana ridi
27	166.4	8.3	282	4	AF132081	AF132081 Ictalurus
28	160.4	8.0	1410	3	AF025411	AF025411 Oryctolag
29	159.6	8.0	1703	91	HSU28281	U28281 Human secre
30	158	7.9	1616	91	HSU13989	U13989 Human secre
31	156.4	7.8	1650	91	HSU20178	U20178 Human secre
32	156.2	7.8	1377	5	I28734	I28734 Sequence 1
33	156.2	7.8	2836	3	SSU49434	U49434 Sus scrofa
34	146.2	7.3	2348	92	HUMVAIPR	L20295 Homo sapien
35	146.2	7.3	2754	92	HUMVAPR	L13288 Human vasoa
36	143.8	7.2	1796	5	E04128	E04128 cDNA encodi
37	143.8	7.2	1796	12	RNSECRS	X59132 R.norvegicu
38	140.4	7.0	548	91	HSPTHR03	U47127 Human parat
39	139.6	7.0	2224	4	AF048819	AF048819 Carassius
40	138.8	6.9	2592	4	CAU56391	U56391 Carassius a
41	137.8	6.9	1654	4	MGU31391	U31391 Meleagris g
42	137.8	6.9	2109	4	AB029895	AB029895 Gallus ga
43	137.8	6.9	3129	5	E05551	E05551 DNA encodin
44	137.8	6.9	3129	12	RATVASREC	M86835 Rat vasoeac
45	134.6	6.7	506	4	AF100643	AF100643 Rana ridi

ALIGNMENTS

RESULT	1	HSU25128	2641 bp	PR1	06-JUL-1995
LOCUS		Human PTH2 parathyroid hormone receptor mRNA, complete cds.			
DEFINITION		U25128			
ACCESSION		U25128			
VERSION		U25128.1			
KEYWORDS		human.			
SOURCE		human.			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS		Udlin,T.B., Gruber,C. and Bonner,T.I.			
TITLE		Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor			
JOURNAL		J. Biol. Chem. 270 (26), 15455-15458 (1995)			
MEDLINE		95318121			
REFERENCE		2 (bases 1 to 2641)			
AUTHORS		Bonner,T.I.			
TITLE		Direct Submission			
JOURNAL		Submitted (17-APR-1995) Tom I. Bonner, Lab of Cell Biology, NIMH, Bldg. 36, Room 3A-17, Bethesda, MD 20892-4090, USA			
FEATURES		Location/Qualifiers			
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		/db_xref="taxon:9606"			
		/tissue_type="cerebral cortex and hippocampus"			
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		/note="G protein-coupled receptor"			
		/codon_start=1			
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		/product="PTH2 parathyroid hormone receptor"			
		/protein_id="AAC50157.1"			

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CNPNGTDFMHSILNKTWANSYSDCLRFLOPDISIGKOEFFERLYVMYTYGYSISFGLA		670 a	564 c	623 g		
VAILIIGFRHLCHTRNTYIMHLPVSFMRATYSIFVKDVRVHAHIGVLESLIMQDD		784 t				
PONSIEATSVDKSQYIGCKIAVVMFIYELATNYWLVLEGLIHLNLFVAFPSDTKYL		ORIGIN				
WGFILIGMFPAAVFAWAVARATLADARCELWSAGDIKIYQAPILAAIGLNFILFL						
NTVRVLA*IKWETNAVGHDRKQYRLAKRSLTLVLVLFVGVHYIVFVCLPHSFTGLGWE						
IRMICELFNSFOGFFVSIYYCNGEVOAQQVKKWSPNLSVDMKRTPPGCSRRGCS						
VLTIVYTHSSQSQAASRASTRMVLISGKAAKIASRQPDSSHITLPGYVWNSSEQDCLPHS						
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	Best Local Similarity	99.0%;	Pred. No. 0;			
	Matches 1975;	Conservative	0;	Mismatches 18;	Indels 2;	
				Gaps 2;		
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DB	63	GGCCAGCCCAAGTTGGCACTTGGAACTTCTCCCGGCTCTGGAGGAGGTCCCTGCTTC	122			
QY	70	ttcctacagccgttcgggcatggcgctggcgctgcctccacgtctctgggttgc	129			
DB	123	TTCTCTACACCGTTCGCGGCATGGCGGCTGGGGCTCCACGCTCTGGGGTTGCG	182			
QY	130	taatctcgccagctgctcctggcagagccagctggattctgagcaccatacta	189			
DB	183	TAATGCTCGGACGTCGCTCCTGGCCAGAGCCAGCTGGATTCTGATGGCACCATTA	242			
QY	190	tagagagcagattgtcctgtgctgaaagcagaagtacaaatgtgaactcaacatacag	249			
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QY	250	ctcaactccagagagaggaaggaattgttccctgaaatggatggactcatttgttgc	309			
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QY	430	gcttaataaaacatgggccaattattcagaactgccttcgcttctgcagccagatata	489			
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QY	490	gcataaggaagcaagaattctgtgaacgctctatgtataatgccttggtgactcca	549			
DB	543	GCATAGGAAGCAAGAAATCTTTGACGCGCTCTATGTAATGTATACCGTTGGCTACTCA	602			
QY	550	tctcttttggttccctggctgtggctattctcatcatattggttacttcagacagattgcatt	609			
DB	603	TCCTTTTGGTTCTTGGCTGTGGCTATTCTCATCATTTGTTACTTCAGACGATTCGATT	662			
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QY	670	tctttgtcaaacagagtagtccatgctcacataggagtagaagagctgggtgctccctaa	729			
DB	723	TCCTTTGTCAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGGAGTCCCTAA	782			
QY	730	taatgcagatgacccacacaaaaattccattgagggcaactctctgtggacacaaatcacata	789			
DB	783	TAATGAGGATGACCCACAAAATTCATTGAGGCAACTTCTGTGGCAAAATCACAATATA	842			

Query Match				97.0%;	Score 1942.2;	DB 93;	Length 2641;
Best Local Similarity				99.0%;	Pred. No. 0;		
Matches 1975;				Conservative	0;	Mismatches	18;
						Indels	2;
						Gaps	2;
Qy	10	gggcacgaagttgcataattgaagcttttccgggctctgagagggtccctgcttc	69				
Db	63	GGCCAGCCAAAGTTGGCACTTGGAAAGCTTCTCCGGGCTCTGGAGAGGGTCCCTGCTTC	122				
Qy	70	ttctacagccgtctccgggcatggcctgggtggggtcgctccacgtctctgggttggc	129				
Db	123	TTTCTACAGCCGTTCCGGGCATGGCGGCTGGGGGCTCGCTCCACGCTCTGGGGTTGGC	182				
Qy	130	taatctcgccagctgctccctggccagagccagctggattctgatggacatacta	189				
Db	183	TAATGTCGCCAGCTGCCYCCYGGCCAGAGCCAGCTGGATTCTGATGCGACCAATTACTA	242				
Qy	190	tagaggagcagattgtccctgtgctgaaagcgaagtaagtaacatgtaactcaacatacag	249				
Db	243	TAGAGGAGCAGATTGTCTTGTGCTGAAGCGAAAGTACAATGTGAACCTCAACATCAGAG	302				
Qy	250	ctcaactccaggaggaggaagtaattgtttccctgaaaggagtggaactcatttgttggc	309				
Db	303	CTCAACTCAGGAGGAGAGGTAATTGTTTCCYGAATGGGATGGACTCAITTTGTTCGC	362				
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Qy	370	accataaaggagttgtcttccagactgtaaccccaatggaaacatgggattttatgcaca	429				
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Qy	730	taatgcagatgaaccacaaaattccattgaggaacttctgtgacaaaatacacata	789				
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RESULT 3

RNU55836

LOCUS

DEFINITION

Rattus norvegicus parathyroid hormone receptor mRNA, complete cds.

19-OCT-1996

ROD

PTH2

hormone receptor

PTH2

complete

[illegible]

551	Db	ATTATATGGGCTCAAAATAAAACCTGGGGCTAACTATTTCAGACT-----GCTTTCTGCAGCCT	604
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 159700)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-3M22
Unpublished
2 (bases 1 to 159700)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-SEP-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2000 this sequence version replaced gi:6454017.
All repeats were identified using RepeatMasker:
Smith, A. F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2778
Center clone name: 3.M.22
----- Summary Statistics
Sequencing vector: M13; W77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145599 bases at least Q40
Consensus quality: 151691 bases at least Q30
Consensus quality: 154613 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 158500; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs

TITLE
JOURNAL
COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1067: contig of 1067 bp in length
* 1068 1167: gap of 100 bp
* 1168 5145: contig of 3978 bp in length
* 5146 5245: gap of 100 bp
* 5246 11674: contig of 6429 bp in length
* 11675 11774: gap of 100 bp
* 11775 16018: contig of 4244 bp in length
* 16019 16118: gap of 100 bp
* 16119 22143: contig of 6025 bp in length
* 22144 22433: gap of 100 bp
* 22434 29636: contig of 7393 bp in length
* 29637 29736: gap of 100 bp
* 29737 37603: contig of 7867 bp in length
* 37604 37703: gap of 100 bp
* 37704 47116: contig of 9413 bp in length
* 47117 47216: gap of 100 bp
* 47217 61066: contig of 13850 bp in length
* 61067 61166: gap of 100 bp

* 61167 80698: contig of 19532 bp in length
* 80699 80798: gap of 100 bp
* 80799 103166: contig of 22368 bp in length
* 103167 103266: gap of 100 bp
* 103267 129867: contig of 26601 bp in length
* 129868 129967: gap of 100 bp
* 129968 159700: contig of 29733 bp in length.

FEATURES

Location/Qualifiers

source

1. 159700

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="RP11-3M22"

/clone_lib="RPC1-11 Human Male BAC"

1. 1067

/note="assembly_fragment"

1168. 5145

/note="assembly_fragment"

5246. 11674

/note="assembly_fragment"

11775. 16018

/note="assembly_fragment"

16119. 22143

/note="assembly_fragment"

22244. 29636

/note="assembly_fragment"

29737. 37603

/note="assembly_fragment"

clone_end:SP6

vector_side:left

37704. 47116

/note="assembly_fragment"

clone_end:T7

vector_side:right

47217. 61066

/note="assembly_fragment"

61167. 80698

/note="assembly_fragment"

80799. 103166

/note="assembly_fragment"

103267. 129867

/note="assembly_fragment"

129968. 159700

/note="assembly_fragment"

BASE COUNT 50230 a 29925 c 30059 g 48284 t 1202 others
ORIGIN

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Best Local Similarity 98.2%; Pred. No. 9.5e-167;
Matches 648; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
QY 1345 aggttcagcagaggtgaagaagatgtggagtcggtggaatctctcgtgagctggaata 1404
Db 41949 AGGTTACGAGGAGGTGAAGAAGATGTGGAGTCGGTGGAGACCTCTCCGTGACTGGA 41890
QY 1405 ggcacccgcatgtggcagcgcagatgcgctcagtcgctcaccacgcgacgcacagca 1464
Db 41889 GGACACCCCATGTGGCAGCGGAGATGCGGCTCAGTGTCTACCCACCGTACGCGACAGCA 41830
QY 1465 ccagcagccagtcacaggtggcgg-cagcacagcagtcggtgcttatctctgcaaaagctg 1523
Db 41829 CCAGCAGCCAGTCACAGGTGGCGGCCAGCACGCATGGTGTCTATCTCTGGCAAGCTG 41770
QY 1524 ccaagatcgccagcagacagcctgacagccacatcatcttaacctggtatgctgagta 1583
Db 41769 CCAAGATCGCCAGCAGACAGCCTGACAGCCACATCATCTTACCTGGTATGTCTGGAGTA 41710
QY 1584 actcagagcagagtcgctcacacactctctccacagagcagcaagaagagtagtgagg 1643
Db 41709 ACTCAGAGCAGGAGTGGCTGCCACACTCTTTCCACAGGAGGAG-ACCAAGGAAGATAGTGG 41651
QY 1644 aggcagagagatgatattctaagtgagaagccttccaggcctatggaatcaccacagac 1703

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Db 41650 AGGCAGGGAGATGATATTCTAATGGAGAGCCTCCAGGCCCTATGGAATCTAACCCAGAC 41591
QY 1704 actgaaggtgacaagagaaactgagtgcttctgaatgacatgctgctgact 1763
Db 41590 ACTGAAGGATGCCAGGAGAACTAGGATGTTCTGTAATGACATTTGTGGCTGACTT 41531
QY 1764 tcatggctgggtccaatggctggtgtgtgagagggcttggctgatactcctatgcttga 1823
Db 41530 TCATGGCTGGTCCAAATGCTGTTGTGTGAGAGGCTTGGCTGATACCTATGCTTGA 41471
QY 1824 gcacaaagctgaaattcagtttaaggtgttacttaataatagtttttaggtccatgaa 1883
Db 41470 GTTCAAAGCTGAAATTCAGTTAAGGTGTACTTAATAATAGTTTATAGGCTCCATGAA 41411
QY 1884 ttggccctctgtaactactacacatgaaatgcaagtgtcaatgagtagttattacc 1943
Db 41410 TTGGCTCCCTGTTAAATACCAACATGAAATGCCAAGTGTCAATGGAGTAGTTTATACC 41351
QY 1944 ttctattggcatcaagtttctctctaaatgaattatgattgtctctgtgattgttca 2003
Db 41350 TTCTATTGGCATCAAGTTTCTCTCTAAATTAATGATGATATTGCTCTGTGATTGTTC 41291

RESULT 6
AC019185
LOCUS      AC019185      173316 bp      DNA      HTG      16-JUL-2000
DEFINITION Homo sapiens chromosome 2 clone RP11-299P7, WORKING DRAFT SEQUENCE,
9 unordered pieces.
ACCESSION AC019185
VERSION   AC019185.6  GI:9211380
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 173316)
AUTHORS   Waterston,R.H.
TITLE     The sequence of Homo sapiens clone
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 173316)
AUTHORS   Waterston,R.H.
TITLE     Direct Submission
JOURNAL   Submitted (30-DEC-1999) Genome Sequencing Center, Washington
           University School of Medicine, 4444 Forest Park Parkway, St. Louis,
           MO 63108, USA
COMMENT   On Jul 15, 2000 this sequence version replaced gi:8980958.
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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----
Center project name: H_NH0299P07

----- Summary Statistics -----
Sequencing vector: M13; %

Sequencing vector: plasmid; %

Chemistry: Dye-primer ET; % of reads

Chemistry: Dye-terminator Big Dye; % of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 169101 bases at least Q40

Consensus quality: 170008 bases at least Q30

Consensus quality: 170805 bases at least Q20

Insert size: 164000; agarose-fp

Insert size: 172516; sum-of-contigs

Quality coverage: 5.71 in Q20 bases; agarose-fp

Quality coverage: 6.25 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
* be preserved.

* 1 1606: contig of 1606 bp in length

* 1607 1706: gap of unknown length

* 1707 3626: contig of 1920 bp in length

* 3627 3726: gap of unknown length

* 3727 7755: contig of 4029 bp in length

* 7756 7855: gap of unknown length

* 7856 17841: contig of 9986 bp in length

* 17842 17941: gap of unknown length

* 17942 30925: contig of 12983 bp in length

* 30925 31024: gap of unknown length

* 31025 46299: contig of 15275 bp in length

* 46300 46399: gap of unknown length

* 46400 71861: contig of 25462 bp in length

* 71862 71961: gap of unknown length

* 71962 119567: contig of 47606 bp in length

* 119568 119668: gap of unknown length

* 119668 173316: contig of 53649 bp in length.

FEATURES

Source

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="2"

/clone="RP11-299P7"

1. 1606

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/note="assembly_name:Contig13"

3727..7755

/note="assembly_name:Contig14"

7856..17841

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clone_end:17

vector_side:left"

17942..30924

/note="assembly_name:Contig16"

31025..46299

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46400..71861

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71962..119567

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119668..173316

/note="assembly_name:Contig20

clone_end:SP6

vector_side:left"

BASE COUNT 54299 a 32790 c 32650 g 52776 t 801 others

ORIGIN

Query Match 31.0%; Score 620; DB 43; Length 173316;

Best Local Similarity 98.2%; Pred. No. 9.7e-167;

Matches 648; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 1345 aggttcagcagaggtggaagaatgagtcggtggaatctctccgtgactggaata 1404

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Db 154747 AGGTTACGACAGGTGACAGAGATGTGAGTCGGTGGACCTCTCCGTGGACTCGAATA 154806

|||||

QY 1405 ggacaccgccatgtggcagccagatgctcagtcagtcagtcacccacgltgacgcacacga 1464

|||||

Db 154807 GGACACCGCCATGTGGCAGCGCAGATGGGCTCAGTGTCTACCCAGCGTGACGACAGCA 154866

|||||

QY 1465 ccagcagcagtcacaggtgagcggcaggcacacgcatggtgttatctctcgcaagctg 1523

|||||

Db 154867 CCAGACGCGCAGTCACAGGTGGCGGCAGCACACGATGGTGTCTCTGCGCAAGCTG 154926

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QY 1524 ccaagatccagcagcagcagctgacagccacatcacttacctgctatgctgagta 1583

|||||

Db 154927 CCAAGATCCGACAGCAGACAGCCTGACAGCCACATCATTACTTGTCTGTGAGTA 154986

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QY 1584 actcagcagcagctgctcacacactctctccagagagacacaaagaagatagtg 1643

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Db 154987 ACTCAGACGAGACTGCTGCCACACTCTTTCCAGGAGG-ACCAAGGAAGATAGTGGG 155045

Qy 1644 aggcagagagatgatattctaagtgaagaagccttccagggcctatggaatcaaccagac 1703

Db 155046 AGGCAGGAGATGATATTTCTAATGAGAAGCCTTCCAGGCCATATGGAATCTAACCCAGAC 155105

Qy 1704 actgaagagatgacaagaagagaactgagagatgttctctgaatggagcatgtgtggtgactt 1763

Db 155106 ACTGAAGGATGCCAAGAGAGAACTGAGAGATGTTCTCTGAATGGACATTTGTGGCTGACTT 155165

Qy 1764 tcatggcctgctcaatggcctgtgtgtgagagggcttggctgatactcctatgcttga 1823

Db 155166 TCATGGGCTGCTCAATGGCTGTGTGTGTCAGAGGGCTTGGCTCATATCTCCTATGCTTGA 155225

Qy 1824 gcacaaagggctgaaattcaggttaaggtgttacttaataatagtttttttaggctccatgaa 1883

Db 155226 GTTCAAAAGGCTGAAATTCAGTTAAGGTGTGTACTTAATAATAGTTTTTAGCTCCATGAA 155285

Qy 1884 ttggctcctgtaataactaacagacatgaaatgcaagtgtcaatggagtagtctattacc 1943

Db 155286 TTGGCTCCTGTAAATACTAAGCAGCATGAAATGCAATGTCGAATGGAGTAGTTATTACC 155345

Qy 1944 ttctattggcatcaagtttctcctcaattatgtatgtattgtctgtgattgttca 2003

Db 155346 TTCTATTGGCATCAAGTTTCTCTAAATTAATGTATGTTGCTGTGTGATGTGTTC 155405

RESULT 7

AF132082 2429 bp mRNA VRT 29-OCT-1999

LOCUS Danio rerio parathyroid hormone type-2 receptor precursor, mRNA, complete cds.

DEFINITION AF132082

ACCESSION AF132082

VERSION AF132082.1 GI:5805256

KEYWORDS zebrafish.

SOURCE Danio rerio

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora; Danio.

REFERENCE 1 (bases 1 to 2429)

AUTHORS Rubin,D.A., Hellman,P., Zon,L.I., Lobb,C.J., Bergwitz,C. and Juppner,H.

TITLE A G protein-coupled receptor from zebrafish is activated by human parathyroid hormone and not by human or teleost parathyroid hormone-related peptide. Implications for the evolutionary conservation of calcium-regulating peptide hormones

J. Biol. Chem. 274 (33), 23035-23042 (1999)

JOURNAL 93367425

MEDLINE 2 (bases 1 to 2429)

REFERENCE Rubin,D.A., Hellman,P., Zon,L.I., Lobb,C.J., Bergwitz,C. and Juppner,H.

AUTHORS Direct Submission

TITLE Submitted (01-MAR-1999) Endocrine Unit, Wellman 5, Massachusetts General Hospital, Fruit Street, Boston, MA 02114, USA

JOURNAL Location/Qualifiers

FEATURES source

1. .2429

/organism="Danio rerio"

/db_xref="taxon:7955"

/tissue_type="kidney"

103. .1830

/note="5, RACE"

/codon_start=1

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/protein_id="AA051908.1"

/db_xref="GI:5805257"

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IKKTWTNLIADFVKVPCVCSNRYGSLVLTGLNNSTSQSOLAAGGCTRTSTLFSR
VYRSSGGPTVSTHATLPGYVLNSDADSLPPSIPEPEDSAKQVDDILLKESLTPRSS
GLEDEDTL"

BASE COUNT 634 a 555 c 580 g 660 t

ORIGIN

Query Match 29.7%; Score 594.4; DB 4; Length 2429;
Best Local Similarity 64.6%; Pred. No. 1.le-159;
Matches 977; Conservative 0; Mismatches 506; Indels 29; Gaps 5;

Qy 174 gatggaccatcactatagagagagcagattgtccttctgtgtgaagcgaagtaacatgt 233

Db 280 GATGGCAGATTACAGCTGAAGAACACAGGTCAAAATGCTGCTGGATGCAAGCTGCAGTGC 339

Qy 234 gaactcaacatcaacagctcaactccagagaggaagaagtaattgttccctgaatggat 293

Db 340 CTCCAAAAGGTTCCAGCGATGACC---CTGCAGTTGGTGTGTGTCTCCAGAGTGGAT 396

Qy 294 ggactcatttggccccagaggaacagtggggaaaaatctcggtgttcccatgcccctct 353

Db 397 GGTCTGATATCTTGSCCACAAGGCTTCCCTGGGAGCTGACCAAGACACCTGCCTGGA 456

Qy 354 tatatttatgacttcaaccataaaggaggtgtccttccgacactgttaaccccaatggaaca 413

Db 457 TACATCTATGACTTCAACCATGCAGCATGCATACAGAGGCTGTGACTCTAATGGTTCC 516

Qy 414 tgggattttatgcagcgttaataaaaaatcagggcccaattattcagactgcttgcgttt 473

Db 517 TCGGTGCTGGCAGAGAGCTCAACAAGACCTGGGTCAACTACACTGAATGATCAAAAT-- 574

Qy 474 ctgcagccagatatcagcataggaagcaagaattctgtgaagcctctatgtaatgtat 533

Db 575 ----CCCCAGAGCCCAACAAAAGACAGAGCTCTTTTGAACGGCTGCACATCATGTATC 630

Qy 534 accgttggctactccatctcttgggttccttgggtgtggtgttcttctcatcattgggttac 593

Db 631 ACAGTCGGCTATGAGTGTCTTTCAGCTCTCTCTAGTGGCCATCTTTATTATCGGATAT 690

Qy 594 ttcagagatttgcaattgcactaggaactatatacacttgacacttatttgccttcttcag 653

Db 691 TTCAGAGACACTCCACTGCACCAGGAACATACATTCACATGCACCTGTGTTTCTTCTATG 750

Qy 654 ctgagagctacaagcatcttctcaagacagagtaglccatgctcacataggaagaaag 713

Db 751 CTGGTCCGCCACAGCATCTTTGTGAGGATCAGGTGTGTCACACTAGCGCGGGCTGCAG 810

Qy 714 gagctggagtcctcctaataatcagagatgacccacaaattccattgagggcaactctgtg 773

Db 811 GAATCTGATGCTGTGCTCAT---GAATAACTTCACCAATGCTGTGGATGTGGCACCATGTG 867

Qy 774 gacaaatcaacaatatatcggtgcaagattgtctgtgtgattgtttatttacttctgct 833

Db 868 GACATCTCACAGTATATGGGATGTAAGTGCACCGTTTTCCTGCTCATCTATTTCCTGCT 927

Qy 834 acaaatattattgagctcgtgtggaaggtctctacactgcataaactcatcttctgtgct 893

Db 928 ACAAACTACTATTGGATTCCTGGTGAGGGCTTGTACCTGTCAGACAGCTCATCTTCATGGCC 987

Qy 894 ttcttttcggacacaaatacctgtggggcttctcattctgtataggctgggggtttccagca 953

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Qy 954 gcatttctgagcatgggctgtgacgagcaactcgtgctgtatgagctgggtgtctggaa 1013

Db 1048 GTCCTTGTGAGCATGGGCTGTGTGTACAGGCAACACTGGCGGATGCAAGATGCTGGGAG 1107

Qy 1014 cttagtctgagacatcaagtgatttatcaagcaccgactcttagcagctattggcgtg 1073

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Qy 1074 aattttattcttctgaaacacggttagagttcttagctaccacaaatctgggagaccaat 1133

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/product="parathyroid hormone/parathyroid hormone

related-peptide receptor"

367 a 539 g 392 t

BASE COUNT

ORIGIN

Query Match 22.2%; Score 445.2; DB 12; Length 1836;
Best Local Similarity 62.9%; Pred. No. 9.1e-117; Mismatches 423; Indels 15; Gaps 3;
Matches 744; Conservative 0;

QY 265 gagaagtgtaattgttccctgaatggatggactcatattgttggccagagagaacagtgg 324

Db 356 GAGGGCGTCCCTGTCTGCCGAGTGGGACAACATCGTTTGCTGGCCNTTAGGGCACCCAG 415

QY 325 gaaaaatcggctgttcacatccctccttattattatgacttcaacataaagagttg 384

Db 416 GTCAAGTGTGGCAGTACCTTCTCCCGATTACATTTATGACTTCAATCACAAAGGCCATG 475

QY 385 ctttcagacactgaacccaatgaacatggattttatgcacagcttaaaaaaat 444

Db 476 CCTACAGACGCTGTGACCCGAATGGCAGTGGGAGTGGTTCCAGGGCACAAACCCGACGT 535

QY 445 gggccaattattcagactgccttcgtcttcgcagccagatatacagcataggaaaagcaag 504

Db 536 GGGCCAACTACAGCGAGTGCCCTCAAGTTTCATGACCAATGA-----GAGCGCGAACGGG 589

QY 505 aattctgtgaacgcctctatgtaatgtatccgttggctactccatctcttttggttcct 564

Db 590 AGGTATTTGACCGCCTPAGGCATGATCATACCGTGGGATPACCTCCATGTCTCGCCTCC 649

QY 565 tggctgactattctcactgttacttcagacgattgcatgcactagaaactata 624

Db 650 TCAGGTGGCTGTGCTCATCTCTGGCCATTTTAGGGGGCTGCACGCGCCAACTACA 709

QY 625 tcacatgcacttattgtgttttcactgctgagagctacaagcatctttgtcacaagca 684

Db 710 TCCACATGCACATGTTCTCTGTGTTATGCTGCGCGCGGAGCATCTTCGTGAAGGAGG 769

QY 685 gaggtagcatcgcacatagagtaaaagagctggagtcocataataatgcsggagtcac 744

Db 770 CTGTGCTCTACTCTGGCTTTACGCTGGATGAGGCGCGGCTCACAGAGGAAGAGTTGC 829

QY 745 cacaaaattccattgaagcaactctgtgacaaaac-----acaatatatcgggtgca 798

Db 830 ACATATCCGGAGGTGCCACCTCCGCCGCGCGCTGCGCCCGTAGGCTACGCTGGCTGCC 889

QY 799 agattgctgttgatgtttattacttcctggctacaaaattattattgatacctgggtg 858

Db 890 GCGTGGCGGTGACCTTCTTCTCTACTTCTCTGGCTAGCAAACTACTACTTGATTCGTGGTGG 949

QY 859 aaggtctctacatgataatctcacttctgtgtgttcttcttcgacacccaataacacctg 918

Db 950 ACGGGCTGTACTTGCAACGCTCATCTTCATGGCCCTTTTCTCACAGAAAGAGTACCTGT 1009

QY 919 ggggcttcactcttgatagctggggtttccagcagcatttttgcagcatggcgtg 978

Db 1010 GGGGCTTACCAATCTTGGCTGGGCTACCGGCTGTCTTCGTGGCTGTGTGGGTGGGTG 1069

QY 979 cagagcaactcctggctgagtgagtgctgggaacttagtctgagagacatacaagtga 1038

Db 1070 TCAGAGCAACCTTGGCCAACTAGGTGTGGATCTGAGCTCCGGGACACAAGAGTGA 1129

QY 1039 ttatatcaagcacatctcttagcagctatttgggtgaatttcttctctgataacagg 1098

Db 1130 TCATCAGGTGGCCATCTCCGGCATCTGTGTCTCAACTTCATCTCTTTTATCAACATCA 1189

QY 1099 tttaggttctagctacaaaactctggagagcaaatgacgttgggcatgacaaaggaagc 1158

Db 1190 TCCGGGTGCTTGCCACTAGCTTCGGGAGACCAATGCGGGCGGCTGTGACACCGACG 1249

QY 1159 aatacagaaaactggccaaaatcgacactggtctctggtctcttagtctttggagtcattaca 1218

Db 1250 AGTACGGGAAGAGTGCTCAGGTCACAGTTGGTCTGTCGGCTCTTTGGTGCCACTACA 1309

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QY 1336 gcaatggagaggttcagcgaggtgaagaatgctggagtcggtggaatctctccgtgg 1395

Db 1430 GCAATGGTGAGGTGCAGCGAGAGATTAGGAAGTCATGAGCGCTGGACACTGGCGTTGG 1489

QY 1396 actggaaaaggacacccgcctatgtggcagccgcagatgcggt 1437

Db 1490 ACTTCAAGCGCAAGCAGAGTGGGAGTAGCAGCTACAGCT 1531

RESULT 13

117766

LOCUS

117766

Sequence 3

2051 bp

DNA

PAT

07-OCT-1996

ACCESSION

117766

VERSION

117766.1

GI:1598121

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 2051)

AUTHORS

Segre,G.V., Kronenberg,H.M., Abou-Samra,A., Juppner,H., Potts,J.T.

Jr. and Schipani,E.

TITLE

DNA and vectors encoding the parathyroid hormone receptor,

transformed cells, and recombinant production of PTHR proteins and

peptides

JOURNAL

Patent: US 5494806-A 3 27-FEB-1996;

FEATURES

Location/Qualifiers

1..2051

/organism="unknown"

BASE COUNT

429 a 575 c 616 g 431 t

ORIGIN

Query Match 22.2%; Score 445.2; DB 5; Length 2051;
Best Local Similarity 62.9%; Pred. No. 9.3e-117; Mismatches 423; Indels 15; Gaps 3;
Matches 744; Conservative 0;

QY 265 gagaagtgtaattgttccctgaatggatggactcatattgttggccagagagaacagtgg 324

Db 383 GAGGGCGTCCCTGTCTGCCGAGTGGGACAACATCGTTGTGCTGGCCATTAGGGCACCCAG 442

QY 325 gaaaaatcggctgttcacatccctccttattattatgacttcaacataaagagttg 384

Db 443 GTGAAGTGTGGCAGTACCTTGTCCCGATTACATTTATGACTTCAATCAAAAGGCCATG 502

QY 385 ctttcgacactgaacccaatgaacatggattttatgcacagcttaaaaaaat 444

Db 503 CCTACAGACGCTGTGACCGCAATGGCAGCTGGGAGGTGGTTCCAGGGCACACCCGACGT 562

QY 445 gggccaattattcagactgccttcgtcttctgcagccagatatacagcataggaaaagcaag 504

Db 563 GGGCCAACCTACAGCGAGTGCCTCAAGTTTCATGACCAATGA-----GAGCGGGGAACGGG 616

QY 505 aattctgtgaacgcctctatgtaatgtatccogttggctactccatctcttttggttcct 564

Db 617 AGGTATTTGACCGCCTTAGGCATGATCTACACCGTGGGATACCTCATGTCTCTCGCTCC 676

QY 565 tggctgtgctattctcatcattgttacttcagacgattgcatgcaactaggaactata 624

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 2065)
 AUTHORS Abou-Samra,A.-B., Jueppner,H., Force,T., Freeman,M.W., Kong,X.-F., Schipani,E., Urena,P., Richards,J., Bonventre,J.V.,

Potts,J.T., Kronenberg,H.M. and Segre,G.V.
 Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone related peptide from rat osteoblast-like cells:
 A single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases
 Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736 (1992)
 92212903
 Complete title:
 Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone-related peptide from rat osteoblast-like cells: A single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases intracellular free calcium.
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DEFINITION M.musculus mRNA for parathyroid hormone/parathyroid hormone related peptide receptor.
ACCESSION X78936
VERSION X78936
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SOURCE house mouse.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1984)
AUTHORS Karperien.M., Van Dijk.T.B., Hoeljmakers.T., Cremers.F., Abou-Samra.A.B., Boonstra.J., De Laat.S.W. and Defize.I.H.K.
TITLE Expression pattern of parathyroid hormone/parathyroid hormone

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related peptide receptor mRNA in mouse postimplantation embryos
indicates involvement in multiple developmental processes
Unpublished
2 (bases 1 to 1984)
AUTHORS Karperien.M.
DIRECT SUBMISSION
JOURNAL Submitted (21-APR-1994) M. Karperien, The Netherlands Inst. of
Developmental, Biology, Uppsalaalan 8, 3584 CT Utrecht, NETHERLANDS
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PI Li Y, Rosen CA, Ruben SM, Soppet DR;
XX WPI: 1997-043068/04.
DR P-PSDB; W12695.
XX
XX Human G-protein parathyroid hormone receptor, HLTG74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
PS Claim 1; Fig 1A-E; 62pp; English.
XX
CC A cDNA clone (T53619) codes for a 7-transmembrane receptor (W12695)
CC which has been identified as a human G-protein parathyroid hormone
CC (PTH) receptor, designated HLTG74. It was isolated from a human T
CC cell lymphoma tissue cDNA library. The cDNA can be utilised in the
CC prodn. of recombinant HLTG74 and to design probes e.g. to detect
CC mutations in the receptor gene. Gene therapy methods can be used to
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism and
CC chronic tetany by stimulating an increase in serum calcium levels.
CC Antisense constructs can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphataemia, kidney stone, nephroliasis.
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QY 1021 ctggagacatcaagtggatttatcaagcaccgatcttagcagctattgggctgaatttta 1080
DB 1021 ctggagacatcaagtggatttatcaagcaccgatcttagcagctattgggctgaatttta 1080
QY 1081 ttctgttttctgtaacggttagagttcttagctaccaaaatctgggagaccaaatgcagttg 1140
DB 1081 ttctgttttctgtaacggttagagttcttagctaccaaaatctgggagaccaaatgcagttg 1140
QY 1141 ggcattgacacaaaggagcaaatacagaaaactggcacaatcgacactggtctctggctcctag 1200
DB 1141 ggcattgacacaaaggagcaaatacagaaaactggcacaatcgacactggtctctggctcctag 1200
QY 1201 tcttggagtgcatcacatcggttctgtgctgcctcactcctcactgggctggctgggt 1260
DB 1201 tcttggagtgcatcacatcggttctgtgctgcctcactcctcactgggctggctgggt 1260
QY 1261 gggagatccgatgcactgtgagctcttcttcaactccttccagggttcttctgtgtcta 1320
DB 1261 gggagatccgatgcactgtgagctcttcttcaactccttccagggttcttctgtgtcta 1320
QY 1321 tcatctactgtactgcaatggagaggttccagcagaggtgaaagaatgtgagatcggt 1380
DB 1321 tcatctactgtactgcaatggagaggttccagcagaggtgaaagaatgtgagatcggt 1380
QY 1381 ggaatctctccgtggactggaaaagacaccccgatgtggcagccgagatcgcgctcag 1440
DB 1381 ggaatctctccgtggactggaaaagacaccccgatgtggcagccgagatcgcgctcag 1440
QY 1441 tgcctcaccacgtgcagcacagcaccagcagccagtcacagtggtggcgagcacacgat 1500
DB 1441 tgcctcaccacgtgcagcacagcaccagcagccagtcacagtggtggcgagcacacgat 1500
QY 1501 ggggttatactctggcaagctgccaagatgccagcagagagcgtgcagacacatac 1560
DB 1501 ggtgtctatctctggcaagctgccaagatgccagcagagagcgtgcagacacatac 1560
QY 1561 ttctactggtctatgtctggagtaactcagagcagactcctcacacactctctccaga 1620
DB 1561 ttctactggtctatgtctggagtaactcagagcagactcctcacacactctctccaga 1620
QY 1621 ggagcaacaaggaaagatagtgggagcgagagatgtatattcttaattggagaagccttcca 1680
DB 1621 ggagcaacaaggaaagatagtgggagcgagagatgtatattcttaattggagaagccttcca 1680

Db 1621 ggagcaacaggaagatagtggggagagagatgtattcttaagtgaagccttcca 1680
Qy 1681 ggcctatggaatctaacccagacactgaagatgacaagggagaactgagatgttctct 1740
Db 1681 ggcctatggaatctaacccagacactgaagatgacaagggagaactgagatgttctct 1740
Qy 1741 gaatggacatgtggtgactttcatggtgctggtcccaatggtggtgtgtgagagggc 1800
Db 1741 gaatggacatgtggtgactttcatggtgctggtcccaatggtggtgtgtgagagggc 1800
Qy 1801 ttgctgaactcctatgcttgagcacacaagagctgaaaattcagtttaagtgttacttaa 1860
Db 1801 ttgctgatacctcctatgcttgagcacaaaagctgaaaattcagtttaagtgttacttaa 1860
Qy 1861 taatagtttttaggctccatgaattggtcctctgtaataactaacgacatgaaatgcaag 1920
Db 1861 taatagtttttaggctccatgaattggtcctctgtaataactaacgacatgaaatgcaag 1920
Qy 1921 tgtcaatggagtagttattacccttctattggtcctcattggtcctcctctaaattatgtat 1980
Db 1921 tgtcaatggagtagttattacccttctattggtcctcattggtcctcctctaaattatgtat 1980
Qy 1981 ggtattgctctgattgttcca 2003
Db 1981 ggtattgctctgattgttcca 2003
RESULT 2
T15945
ID T15945 standard; cDNA; 1862 BP.
XX AC T15945;
XX
XX 18-MAY-1996 (first entry)
XX DE Opossum kidney PTH/PTHrP receptor cDNA clone OK-H.
XX KW Parathyroid hormone; receptor; parathormone; PTH;
XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
XX KW hypercalcaemia; hypocalcaemia; cancer; opossum; transgenic animal;
XX KW transgenic fowl; ds.
XX OS Didelphis virginiana.
XX XX
XX FH Key Location/Qualifiers
XX CDS 98..1645
XX FT /*tag= a
XX PN US5494806-A.
XX XX
XX PD 27-FEB-1996.
XX XX
XX PF 05-APR-1991; 91US-0681702.
XX XX
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX XX
XX PA (GENO) GEN HOSPITAL CORP.
XX XX
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX XX
XX DR WPI: 1996-139028/14.
XX DR P-PSDB: R92275.
XX XX
XX PT DNA encoding vertebrate parathyroid hormone receptor - useful for
XX PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
XX PT cancer etc.
XX XX
XX PS Claim 1; Fig 1A-1E; 64pp; English.
XX XX
XX CC A cDNA clone (T15945), designated OK-H ATCC 68573), codes for a
XX CC parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)

CC receptor (R92275). To obtain OK-H, an opossum kidney (OK) cell cDNA
CC library in pCDNA1 was used to transfect COS cells, and transfectants
CC were selected for ability to bind labelled PTH. Another cDNA clone,
CC OK-O (T15946), was also isolated in this screening; OK-H and OK-O
CC may represent 2 separate genes or may result from a laboratory
CC artifact. Recombinant receptors are produced in vector/host cell
CC systems. The host cells can also be used for diagnostic measurement
CC of PTH serum levels. Transgenic chickens that overexpress the
CC receptor in their oviduct lay eggs of higher calcium content.
XX
SQ Sequence 1862 BP; 408 A; 495 C; 521 G; 438 T; 0 other;

Query Match 22.6%; Score 452.6; DB 17; Length 1862;
Best Local Similarity 63.0%; Pred. No. 1.7e-134;
Matches 752; Conservative 0; Mismatches 429; Indels 12; Gaps 3;
Qy 257 ccagagggagagaagtaattgtttccctgaaatggagtggaactcatttgggcccaagg 316
Db 391 ccggtcgcagatggtcttctgcctacatgagtggaacaacattgtgtgctgctgctgg 450
Qy 317 aacagtggggaataatcgctgttccatgccctccttatattatgacttcaaccataa 376
Db 451 agtccccggcaaggtgtggtgctgccccgactacttctacgacttcaaccacaa 510
Qy 377 aggagtgtcttccgacactgtaaccccaatggaaacatggattttatgcacagcttaa 436
Db 511 agccgagcctatcggtgtgacagcaatggcagctgggagctggtgctgggaacaa 570
Qy 437 taaaacatgggccaattattcagactgccttcgcttcttctgagccagatatacagatagg 496
Db 571 ccggacatggcggaattacagcgaatgtgtcaagttgtcaccacagagacc-----cg 624
Qy 497 aaagcaagaattctgaaacgcctctatgtaattatataccttggtcactcactctctt 556
Db 625 ggaacgggaagctcttgatcgccctcggaatgatctacactgtgggtactcctctct 684
Qy 557 tggctctggtgctggtctattctcattgttacttcagacgattgtgcactag 616
Db 685 gggctcctcactggtgctggtgattctggttactttaggaggttactatgcaccg 744
Qy 617 gaactatcacatgcacttattgtgtcttcttcagtctgagagctacacagctcttgt 676
Db 745 aaactacattcacatctctctgctcttcttctgtcgcgggtgtaagcatctctat 804
Qy 677 caagacagagtagtccatgctcacataggagtaaaaggagctggagtccttaataatgca 736
Db 805 caaggatgctgtctctactcgggggtttccacagatgaaatcagag---cgcatcacga 861
Qy 737 ggtgaccccaaaaattccattgaggcaactctctgtgacaatacacaaatatacgggtg 796
Db 862 ggagagctgagggccttcacagagcctccctctgctgacaaggcgggtttgtggtgctg 921
Qy 797 caagattgctgtgtgatgtttattactctcctggtcacaataattattatggactcctgt 856
Db 922 cagagtggcggtaaacgcttctccttactctgaccaccaactactactggtactcctggt 981
Qy 857 ggaaggtctctacatgataataatcattcttgggtcttcttcttcggacacccaataact 916
Db 982 ggaaggcctctacatcaccagcctcattctcatggcttttctctcgagaaaagtatct 1041
Qy 917 gtggggtctcattgtgataggctgggggtttccagcagcagcattttgtgcagcatgggctg 976
Db 1042 ctgggggtttcacattattgtggtggtggtcctccctgctggtggtggtggtgac 1101
Qy 977 ggcacgacgaactctggtgatgctgaggtgctgggaacttagtctgtagacatacaagt 1036
Db 1102 cgtgagggtacactggccaacactgagtgtgctggacctgagttcgggggaataagaatg 1161
Qy 1037 gatttataacagcaccgatctcttagcagctatttgggtgaattttattctgttctgaatac 1096
Db 1162 gatcatacaggtgcccatcctggcagctattgtgtggaactttattctttttcaatat 1221

Db 1402 gcaatgaaatccttcaattcattccagggaatttcctggtgcatatatactgttt 1461
QY 1334 ctgcaatggagaggttcacgcagagaggtgaagaagatgtgagtcggtggaatctccgt 1393
Db 1462 ctgcaatggagaggttcacgcagagagatcaagaagtcagtgaagccgtggaacctggcctt 1521
QY 1394 ggactggaagagacaccgccatgtggcagccgcagatcggtcagtgctca 1446
Db 1522 ggactlcaagcggaagcccgagtgccagcagctacagctatggcccca 1574

RESULT 7

Q29604
ID Q29604 standard: cDNA: 1862 BP.

AC Q29604;

XX 16-MAR-1993 (first entry)

XX Opossum kidney PTH/PTHrP receptor clone, OK-H.

XX Parathyroid hormone; related protein; calcium; antagonist;
antibodies; hypercalcaemia; ss.

OS Didelphis virginiana.

XX Key Location/Qualifiers
FH 98..1645
FT CDS /*tag" a

XX W09217602-A.

XX 15-OCT-1992.

XX 06-APR-1992; 92WO-US02821.

XX 05-APR-1991; 91US-0681702.

PR 06-APR-1992; 92US-0864475.

XX (GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;

PI Segre GV;

XX WPI: 1992-366271/44.

DR P-PSDB; R27704.

XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours

XX Claim 2: Fig 1: 91pp; English.

XX Total RNA was isolated from opossum kidney (OK) cells and used to
CC prep. a cDNA library. The resultant phage libraries were used to
CC transform E. coli contg. a larger helper plasmid p3. The cells were
CC screened to isolate those expressing functionally intact OK cell
CC parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor proteins, performed according to Gearing et al., (EMBO J.
CC 8: 3676, 1989), by identifying colonies capable of binding a
CC suitable radiolabelled ligand. The clone encodes a protein which
CC may be used in a therapeutic compsn. to inhibit activation of PTH or
CC PTHrP and thus reduce the level of calcium in the blood. Cncls.
CC capable of competing with PTH or PTHrP for binding can be identified
CC using the protein prod. and DNAs homologous to PTH DNA can be
CC identified using fragments of the clone as probes. The sequence
CC may be used for the prodn. of antibodies useful for the treatment,
CC classification, prognosis and/or treatment of disorders related to
CC the interaction between a cell receptor and a ligand such as in
CC hypercalcaemia. See also Q29605-11.

XX Sequence 1862 BP; 407 A; 497 C; 520 G; 438 T; 0 other:

XX SQ

Query Match 22.5%; Score 451; DB 13; Length 1862;
Best Local Similarity 63.0%; Pred. No. 5 4e-134;
Matches 751; Conservative 0; Mismatches 430; Indels 12; Gaps 3;

QY 257 ccaggaggagagaaggttaattgtttccctgaaatgggagtggaactcattttgttgcccgagag 316
Db 391 ccgctgcagagatggcttctgctactactgagtgggacaacattgtgtgctggcctgctgg 450
QY 317 aacagtggggaaaaatatcgctgttccatgcctcctctattattatgaacttaaacataa 376
Db 451 agtgcgccggcaaggtggtggtgcctgcctgcctgcctgcctgcctgcctgcctgcctgc 510
QY 377 aggagttgctttccgacactgtaaccccccaatggaacatgggattttatgcacagcttaa 436
Db 511 aggcgagcctatcggcgctgtgacagcaatggcagctgggagctgggtgcttgggaacaa 570
QY 437 taaacatgggccaattattcagactgccttcgcttcttcgagccagatatcagcatagg 496
Db 571 ccggacatgggcgaattacagcgaaatgtgtcaagtcttcgaccaacagagacc-----cg 624
QY 497 aaagcaagaattctgtgaacgctctatgtaatgtatcogtggctactccactctctt 556
Db 625 ggaacgggaagtctttgatcgcctcggaatgatctacactgtggctactccactctct 684
QY 557 tggttccttggctgtgctattctcactcattgtgttacttcagacagattgcattgcactag 616
Db 685 gggctcctcactgtggtgctgctgattcttgggttactttaggaggttaccattgcaccgg 744
QY 617 gaactataccacatgcacttattgtgtcttcttcagctgtgagactcacaagcatctttgt 676
Db 745 aaactacattcacatgcactctcttgccttgccttgcctcgggctgaagcatcttcat 804
QY 677 caaagacagagtagtccatgctccatagaggagtaaaaggagctggagccctccataataatga 736
Db 805 caaggatgctgtctactcgggggtttccacagatgaatcgag---cgcatcaccca 861
QY 737 ggaatgacccacaaaattccatgaggaactctgtggacaatcacaatatatcgggtg 796
Db 862 ggaaggagctgaggggccttcacagagcctccctcctgcctgacaaagggggttttgtgggctg 921
QY 797 caagatgctgtgtgatgtttatttacttctcctggctacaaaattatttggactccttgt 856
Db 922 cagagtggcggtaaacogtctcttacttctcctgacacaaactactactgcatccttgt 981
QY 857 ggaaggtctctacctgcataataatctcttctgtggtcttcttcttgggacacaaaatacct 916
Db 982 ggaaggcctctaccttcacagcctcatcttcctggtttttctctctgagaaaaagtatct 1041
QY 917 gtggggcttcatcttgataggtgggggtttccagcagcatcttgttgagcatgggctgt 976
Db 1042 ctgggggtttcacattatttggctggggcctccctcctgcctgtgtgtgtgtgtgtgtgtgt 1101
QY 977 ggcacgagcaactcctggctgatgcgaggtgtctgggaacttagtctgggagacatacaagt 1036
Db 1102 cgtgggggtcacactggcccaacactgagtgctgggacctgagttcggggaataagaata 1161
QY 1037 gattatcaagcacogactttagcagctattgggctgaattttattctgttcttgaatac 1096
Db 1162 gatcacaggtgcccactcctgagctattgtgtggaactttattctttttatcaatat 1221
QY 1097 ggttagagcttctagctacaaaattcggagaccactcagttgggcatgacacacaaggaa 1156
Db 1222 aatcagagtccttggctactaaactccgggagaccataatgagggagagatgtgcacaggg 1281
QY 1157 gcaatcacaggaactggccaaatcgacactggtcctggtccttagtcttgggagtgatt 1216
Db 1282 acagtataaagcgtgtagtccacgctagtctcctcagcgtctatttggggtgcacta 1341
QY 1217 catcgtgtctgtgtcctgcctcactcctct---tcactgggctcgggtgggagatccgat 1273
Db 1342 catcgtcttcatggccacgcctgtacacagaagtatcaggggttcttggcagtgccaat 1401


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QY 1336 gcaatggagaggttcaggcagaggtgaaagaatgtggagtcggtggaatctctccgtgg 1395
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1457 gcaatggtgaggtgcagcagagattaggaagtcattggagcgcgtggacacgtgggtgg 1516

QY 1396 actggaagacacacgcacatgtggcagccgcagatgcgctt 1437
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1517 acttcaagcgaagcacgaagtggagtagcagctacagct 1558

RESULT 9
V08390
ID V08390 standard; DNA; 2051 BP.
XX
AC V08390;
XX
DT 08-FEB-1999 (first entry)
XX
DE Parathyroid hormone receptor R15B coding sequence.
XX
KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; rat; ds.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 73..1848
FT /tag= a
XX
PN US5840853-A.
XX
PD 24-NOV-1998.
XX
PF 06-JUN-1995; 95US-0471494.
XX
PR 06-APR-1992; 92US-0864475.
PR 05-APR-1991; 91US-0681702.
PR 06-JUN-1995; 95US-0471494.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX
WPI: 1999-034124/03.
DR P-PSDB; W73316.
XX
PT Antibody to parathyroid hormone receptor - for diagnostic or
PT therapeutic use
XX
PS Claim 6; Fig 3; 63pp; English.
XX
CC This sequence encodes the rat parathyroid hormone (PTH) receptor
CC R15B, which is targeted by the antibody of the invention. The antibody
CC of the invention is immunoreactive with naturally occurring human, rat
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia.
XX
SQ Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 other;
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Query Match 22.2%; Score 445.2; DB 20; Length 2051;
Best Local Similarity 62.9%; Pred. No. 4.2e-132;
Matches 744; Conservative 0; Mismatches 423; Indels 15; Gaps 3;

QY 265 ggaaggaatgtttccctgaatggatggactcaattgttgccagaggaacagtgg 324
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 gagggcgctccctgtctgcccagtgaggacaacatcgtttgtgcccattaggggcaccag 442

QY 325 gaaaaatacgcgtgtccatgccctccctattattatgacttcaaccataaagagttg 384
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 gtgaagtggtgcagtagcttcccgattacattattatgacttcaatcaacaaaggccatg 502
```

RESULT 10	
Q29606	
ID	Q29606 standard; cDNA; 2051 BP.
AC	Q29606;
AC	Q29606;
DT	16-MAR-1993 (first entry)
XX	
DE	Rat bone PTHrP/PTHrP receptor clone, R15B.
XX	
XX	
KW	Parathyroid hormone; related protein; calcium; antagonist;
KW	antibodies; hypercalcaemia; ss.
XX	
OS	Rattus rattus.
XX	
FT	Key
FT	Location/Qualifiers
FT	73..1848
FT	/*tag= a
XX	
PN	W09217602-A.
XX	
PD	15-OCT-1992.
XX	
PF	06-APR-1992; 92WO-US02821.
XX	
PR	05-APR-1991; 91US-0681702.
PR	06-APR-1992; 92US-0864475.
XX	
PA	(GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX	
PI	Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI	Segre GV;
XX	
DR	WPI; 1992-366271/44.
DR	P-PSDB; R27706.
XX	
PT	New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT	- for (differential) diagnosis of hypercalcaemia, and diagnosis
PT	and treatment of tumours
XX	
PS	Claim 3; Fig 3; 9lpp; English.
XX	
CC	Total RNA was isolated from rat osteosarcoma (ROS) cells and used to
CC	prep. a cDNA library. The resultant phage libraries were used to
CC	transform E. coli contg. a larger helper plasmid p3. The cells were
CC	screened to isolate those expressing functionally intact ROS cell
CC	parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC	receptor proteins, performed according to Gearing et al., (EMBO J.
CC	8; 3676, 1989), by identifying colonies capable of binding a
CC	suitable radiolabelled ligand. The clone encodes a protein which
CC	may be used in a therapeutic compsn. to inhibit activation of PTH or
CC	PTHrP and thus reduce the level of calcium in the blood. cpds.
CC	capable of competing with PTH or PTHrP for binding can be identified
CC	using the protein prod. and DNAs homologous to PTH DNA can be
CC	identified using fragments of the clone as probes. The sequence
CC	may be used for the prodn. of antibodies useful for the treatment,
CC	classification, prognosis and/or treatment of disorders related to
CC	the interaction between a cell receptor and a ligand such as in
CC	hypercalcaemia. See also Q29604-11.
XX	
SQ	Sequence 2051 BP; 430 A; 576 C; 616 G; 429 T; 0 other;
Query Match	22.1%; Score 442; DB 13; Length 2051;
Best Local Similarity	62.8%; Pred. No. 4.5e-131;
Matches 742; Conservative	0; Mismatches 425; Indels 15; Gaps 3;
QY	265 gagaagtaattgtttccctgaatggagtgactcattgttgcccgagagaacagtgg 324
Db	
QY	383 gaggggccctcgtcgtcccgagcgggacacacatcgtttgtgcccattagggccaccag 442
QY	325 ggaataatagcgtgttccatgcctcttatatttatgacttcaaccataaaggattg 384

Query Match		7.3%	Score 145.4;	DB 13;	Length 1794;
Best Local Similarity		54.6%	Pred. NO. 5.7e-36;		
Matches 365;		Conservative 0;	Mismatches 286;	Indels 18;	Gaps 3;
QY	722	gtccctaataatgcaggatgaccccaaaaattccattgaggcaacttctgtggacaaaatc	781		
DB	780	gtcccaacttcaaaaggacgcgcgtactctctccgcgacgcacactactgtgatgc	839		
QY	782	acaaatatacgggtgcaagatgctgttgatgtgtatttacttctgggtacaaaatta	841		
DB	840	ccataaggctcggctgcaagctggatcatgtctctccagtaactcatcatggccaacta	899		
QY	842	ttattggatccctgggtggaaggctctacatgcataaactcatctttgtggctttctttc	901		
DB	900	cgcattgctgctgggtggaggccctacacttcacacactccttgccatctcctctcttc	959		
QY	902	ggacaccaaaatccctgtgggggttcatcttgatagctggtgggggtttccagcagcatttgt	961		
DB	960	agaaaggaagtacctgcaggccttctgtctctcgatgggttctccagccatttttgt	1019		
QY	962	tgcagcatggctgtggcacgcaactcctgctgatgcgaggtgctggtggaacttagtgc	1021		
DB	1020	tgccttgggtctatcacaggcaactttctagaataactggtgatgctgggacatcaacgc	1079		
QY	1022	---tggagacatcaagtggaatttatcaagcaccgatcttagcagctattgggctgaattt	1078		
DB	1080	caatgcttcctgctgtggtggttcattcgagggcctgtgattctgtccatcctgatcaattt	1139		
QY	1079	tattctgtttctgaatacgggttagagttctagtagtaccaaaatctgggagaccaatgcagt	1138		
DB	1140	catcttcttcaataacattctaagaatcctgatgaggaaacttagaacacaagaacaag	1199		
QY	1139	tgggcatgacacaaggaagcaatacacagaacactggccaaatcgacactgggtcctggtcct	1198		
DB	1200	aggaagtgaaaca---aacattataagcgctggccaaagtccacccctcctgctgatccc	1256		
QY	1199	agcttttgagtgcatatcatcgtgttcgtgtgcctgcctcactcctcctcactgggtcgcg	1258		
DB	1257	gctctttggcatccactacattgtcttcgc-----cttctcccagaggacgc	1304		
QY	1259	gtgggagatccgcgatgcactgtgagctcttcttcaactccttccaggggttcttttgttc	1318		
DB	1305	catggagggtccagctgttcttcgaactggccctgggctccttccaggggtctgtgtggtagc	1364		
QY	1319	tatcatctactgtcactgcaatggagaggttcaggcagaggtgaagaagatgtgaggtcg	1378		
DB	1365	tgtccttactgtcttctcactcaatggtgaggtgcagttggaagttcagaaaaatggcgcca	1424		
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us-09-236-468a-1.rni

Thu Nov 16 15:40:12 2000

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
November 15, 2000, 19:27:28 ; Search time 85.97 seconds
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3523.748 Million cell updates/sec

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Perfect score: 2003
Sequence: 1 gttgctctggcagccaaag.....attgctctgtgattgttca 2003

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues 524120

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/5D_COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2003	100.0	2003	6	PCT-US93-07085-1
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4	452.6	22.6	1862	3	US-08-468-249A-1
5	452.6	22.6	1863	1	US-07-864-249A-2
6	452.6	22.6	1863	3	US-08-468-249A-2
7	445.2	22.2	2051	1	US-07-864-249A-3
8	445.2	22.2	2051	3	US-08-468-249A-3
9	430.4	21.5	2010	1	US-07-864-249A-4
10	430.4	21.5	2010	3	US-08-468-249A-4
11	156.2	7.8	1377	1	US-08-112-817C-1
12	118.8	5.9	1401	3	US-08-855-213-32
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15	118.8	5.9	1869	3	US-08-855-213-40
16	115.2	5.8	2112	5	US-08-845-546-11
17	105	5.2	1455	3	US-08-811-897A-31
18	105	5.2	1455	3	US-08-811-897A-39
19	105	5.2	2730	3	US-08-811-897A-39
20	103.6	5.2	1380	2	US-08-855-213-39
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28	99.2	5.0	1626	2	US-08-381-433A-3	Sequence 3, Appl
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30	97.2	4.9	1862	5	US-09-239-956-14	Sequence 1, Appl
31	97.2	4.9	1875	2	US-08-453-631-14	Sequence 14, Appl
32	97.2	4.9	1875	2	US-08-452-930-14	Sequence 14, Appl
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34	96.4	4.8	1468	6	PCT-US93-0817A-7	Sequence 7, Appl
35	96.4	4.8	1468	2	US-08-381-433A-7	Sequence 1, Appl
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37	96.4	4.8	3012	1	US-08-454-464-1	Sequence 1, Appl
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45	96.4	4.8	3416	1	US-08-454-464-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-468-011A-1
; Sequence 1, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Steven
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2003 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-468-011A-1

Query Match 100.0%; Score 2003; DB 5; Length 2003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1981 GGTATTTGCTCTGTGATGTTCA 2003

RESULT 2
 PCT-US95-07085-1
 ; Sequence 1, Application PC/TUS9507085
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet, Daniel R
 ; APPLICANT: Yi, Li
 ; APPLICANT: Rosen, Craig A
 ; APPLICANT: Ruben, Steven

;> TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
;> TITLE OF INVENTION: HLTG74
;> NUMBER OF SEQUENCES: 8
;> CORRESPONDENCE ADDRESS:
;> ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
;> ADDRESSEE: Stewart & Olstein
;> STREET: 6 Becker Farm Road
;> CITY: Roseland
;> STATE: NJ
;> COUNTRY: USA
;> ZIP: 07068-1739
;> COMPUTER READABLE FORM:
;> MEDIUM TYPE: Floppy disk
;> COMPUTER: IBM PC compatible
;> OPERATING SYSTEM: PC-DOS/MS-DOS
;> SOFTWARE: Patent In Release #1.0, Version #1.30
;> CURRENT APPLICATION DATA:
;> APPLICATION NUMBER: PCT/US95/07085
;> FILING DATE: 05-JUN-1995
;> CLASSIFICATION:
;> ATTORNEY/AGENT INFORMATION:
;> NAME: MULLINS, J. G.
;> REGISTRATION NUMBER: 33,073
;> REFERENCE/DOCKET NUMBER: 325800-393
;> TELECOMMUNICATION INFORMATION:
;> TELEPHONE: 201-994-1700
;> TELEFAX: 201-994-1744
;> INFORMATION FOR SEQ ID NO: 1:
;> SEQUENCE CHARACTERISTICS:
;> LENGTH: 2003 base pairs
;> TYPE: nucleic acid
;> STRANDEDNESS: single
;> TOPOLOGY: linear
;> MOLECULE TYPE: cDNA
;> FEATURE:
;> NAME/KEY: CDS
;> LOCATION: 90..1712
;> PCT-US95-07085-1

Query Match 100.0%; Score 2003; DB 6; Length 2003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1201 TCTTTGGAGTGCAATTACATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
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QY 1981 ggtattgtctgtgattgttca 2003
Db 1981 GGTATTTGCTCTGTGATTTGTCA 2003

RESULT 3

US-07-864-475A-1
; Sequence 1, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; TITLE OF INVENTION: AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1862
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-864-475A-1

Query Match 22.6%; Score 452.6; DB 1; Length 1862;
Best Local Similarity 63.0%; Pred. No. 1.4e-135;
Matches 752; Conservative 0; Mismatches 429; Indels 12; Gaps 3;

QY 257 ccaggaggagagagtaattgtttccctgaatggagatggagcatttgttggcccgagag 316
Db 391 CCGGCTGCAGGATGGCTTCTGCTTACCTAGTGGGCAACATTTGTGTGCTGGCCTGCTGG 450
QY 317 aacagtggggaaaaatatcggtgttccatgcctccttatatttatgacttcaacataa 376
Db 451 AGTGCCCGCAAGGTGGTGGCGCTGCCCTGCCCGACTACTTCTACGACTTCAACACAA 510
QY 377 agagttgtttccgacactgttaacccccaaatggaacatgggatttttatgcacagcttaa 436
Db 511 AGCGCGAGCGCTATCGCGCTGTGACAGCAATGGCAGCTGGAGCTGGTGCCTGGGAACAA 570
QY 437 taaacatggggcaattattcagactgccttcgcttcttcgagccagatatacagcatag 496
Db 571 CCGGACATGGGGCAATTTACAGCGCAATGTGTCAAGTTTCTGACCAACGAGACC-----CG 624
QY 497 aaagcaagaattctgtgaacgctctatgaatgataccgttggctactcctcatcttt 556
Db 625 GGAACGGGAAGTCTTTGATCGCTCGGAATGATCTACACTGTGGGCTACTCCATCTCTCT 584
QY 557 tggttccttggctgggtattctcatcatatggttacttcagacgattgcattgcactag 616
Db 685 GGGCTCCCTCACTGTGGCTGTGCTGATTTCTGGGTACTTTAGGAGGTTACATTGCACCCG 744
QY 617 gaactataccacatgcacttatttggctcttccttccttccttccttccttccttccttcct 676
Db 745 AAACATACATTACATGCATCTCTTCTGCTCTTATGCTCCGGGCTGTAAAGCATCTTCAT 804
QY 677 caaacaacagtagtccatgctcacataggaagagagctggagtcctccttaataatgca 736
Db 805 CAAGGATGCTGTGCTCTACTCGGGGTTTCCACAGATGAATCGAG---CGCATCACCA 861
QY 737 ggatgaccacacaaaattccattgagggcaacttctgtggacaaatcacaaatatatcggtg 796
Db 862 GGAGGAGCTGAGGGCTTTCACAGAGCCTCCCTCTGCTGACAAAGGGGGGTTTGTGGGCTG 921
QY 797 caagattgctgtgtgatttatttatttcttccttccttccttccttccttccttccttcct 856
Db 922 CAGAGTGGGGTAAACGCTCTTCTTACTTCTGACCAACACTACTACTGATCTCTGCT 981
QY 857 ggaaggtctctacctgcataaactcctcttcttcttcttcttcttcttcttcttcttcttct 916
Db 982 GGAAGGCTCTTACCTTTCACAGCCTCATCTTCATGCGCTTTTCTCTGAGAAAAAGTATCT 1041
QY 917 gggggcttctctgtagaggtgggggtttccagcagcatttcttgcagcatgggctgctgct 976
Db 1042 CTGGGTTTTCACATTTATTTGGCTGGGGCTCCCTGCCGTTTGTGCGCTGTGGGTGAC 1101
QY 977 ggcagagcaactctgctgtagtgcagaggtgctgggaacttagtgcggagacatcaagtgc 1036
Db 1102 CGTGAGGGCTACACTGGCCAAACACTGAGTGTGGGACCTGAGTTCGGGGAATAAGAAATG 1161
QY 1037 gatttataagcaccgatcttagcagctattggcctgaattttattcttcttcttcttcttct 1096
Db 1162 GATCATACAGGTGCCCATCTCTGGCAGCTATTGTGGTGAATTTATTTTATCAATAT 1221
QY 1097 ggttagagttcttagctaccaaaatctgggagaccaatgcagttgggcatgacacaggaa 1156

APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF INVENTION: AND DNA ENCODING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/681,702
FILING DATE: 05-04-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/071002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2051
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-07-864-475A-3

Query Match 22.2%; Score 445.2; DB 1; Length 2051;
Best Local Similarity 62.9%; Pred. No. 3.7e-133;
Matches 744; Conservative 0; Mismatches 423; Indels 15; Gaps 3;

QY 265 gagaagtaattgtttccctgaatgggagtggaactcattgttggccagagagaacagtgg 324
DB 383 GAGGGCGTCCCTGTCTGCCCGAGTGGCAACAACATCGTTTGGCTGGCCATTAGGGGCACCG 442
QY 325 ggaataatcggctgtgtccatgcccctcttattattgacttcaaccataaaggagttg 384
DB 443 GTCAAGTGGTGGCAGTACCTTGTCCCGATTACATTTATGACTTCATCAAAAGGCCATG 502
QY 385 ctttcgacactgttaaccccaatgggaactgggattttatgacacgcttaataaaacat 444
DB 503 CTTACAGACGCTGTGACCGCAATGGCAGCTGGGAGTGGTTCCAGGGCACACCGGACCT 562
QY 445 gggccaattatcagactgccttcgcttctcgcagccagatatcagcataggaagaag 504
DB 563 GGCCCAACTACAGCAGTAGTCCCTCAAGTTTCATGACCAATGA-----GACGCGGGAACGGG 616
QY 505 aattctgtgaacgcctctatgtaagtataccgtgtggtactccatctcttttggttct 564
DB 617 AGGTATTGACCGCCTAGGCATGATCTACACCGTGGGATACCTCTCTCGCCCTCCC 676
QY 565 tggctgtggctattctcacaatgttggttactcagacgattgcatgacataggaactata 624
DB 677 TCACGGTGGCTGTGCTCATCTCTGGCCTATTATTAGGGGCTGCACTGCACGCGCAACTACA 736
QY 625 tccacatgcacttatttgttcttccatctgagagcctacaagcalcttctgcaaaagaca 684
DB 737 TCCACATGCACATGTTTCCCTGTCTGCTTTATGCTGCGCGCCGCGAGCATCTTCGTGAAGGACG 796

QY 685 gagtagtccatgctccacataggagtaaaaggagctggagtcctcctaataatgcaggatgacc 744
DB 797 CTGTGCTCTACTCTGTGCTTACGCTGGATGAGGCCGAGCGCTCACAGAGGAAGATTGC 856
QY 745 cacaaaaattccattgaggcaacttctgttgacaaaac-----acaatatatcgggatga 798
DB 857 ACATCATCGCGCAGGTGCCACCTCCGCCCGCGCTGCCGCCGTAGGCTACGCTGGCTGCC 916
QY 799 agattgtgttggatgttatttacttctcctggctacaaaattattattgacctgtgtgg 858
DB 917 GCGTGGCGGTGACCTTCTTCTCTACTTCTCTGCTGCTACCAACTACTACTGGATTCTGGTG 976
QY 859 aaggctctacctgcataaatctcatcttctgtgtgcttcttcttcgggacacaaaataacctgt 918
DB 977 AGGGGCTGTACTTGCACAGCCTCATCTTCATGSCCTTTTCTCAGAGAGAAGTACTCTGT 1036
QY 919 ggggtcttcattgtataggctgggggtttccacagcagcatttcttcagcagcatgggtgtgg 978
DB 1037 GGGGCTTTCACCATCTTTGGCTGGGTCTTACCGCTCTCTTCGTGGCTGTGTGGTGGTG 1096
QY 979 cacagcaactcgtgctgagtgagtgctggaaacttagtggaagacatcaagtga 1038
DB 1097 TCAGAGCAACCTTGGCCAACTGGGTGCTGGGATCTGAGCTCCGGGCAAGAGAGTGGA 1156
QY 1039 ttatcaagcacgcgactcttagcagctattgggctgaattttatctgttcttgaatacagg 1098
DB 1157 TCATCCAGGTGCCCATCTCTGGCATCTGTGTGCTCAACTTCATCTTTTATCAACATCA 1216
QY 1099 tttagagttcagctaccacaaaatctgggagacaaatgcagttgggcatgacacaaagaaac 1158
DB 1217 TCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATCGGGCGCGGTGTGACACGAGGCAGC 1276
QY 1159 aatacagaaactggccaaatgcacactgtcctgtgctagtcttcttgagtgcatata 1218
DB 1277 AGTACCGGAAGTGTCAAGTCCAGTTCAGTTCGCTGCTGCGGCTCTTTGTTGCTCCACTACA 1336
QY 1219 tcgtgttcgtgtgcctgcctcactcc-----ttcactgggctcgggtgggagatcccgatgc 1275
DB 1337 CGCTTTCATGGCTTGCCGTACACCGAGGTCTCAGGACATTTGGGACAGATCCAGATGC 1396
QY 1276 actgtgagctcttcttcaactccttccagggttcttcttctgtctatcatctactgtact 1335
DB 1397 ATTATGAGATGCTTCAACTCTCTCCAGGATTTTCTTCCCATCATATATACTGTTTCT 1456
QY 1336 gcaatggaagattcagcgagaggtgaagaagatgtagagtcgggtggaatctctccgtgg 1395
DB 1457 GCAATGGTGAGGTGAGCGAGAGATTAGGAAGTCATGTGAGCGCGCTGGACACTGGCGTTGG 1516
QY 1396 actggaataaggacacccgcatgtggcagcgcgagatgcggct 1437
DB 1517 ACTTCAAGCGCAAGCACGACGAGTGGGAGTAGCAGCTACAGCT 1558

RESULT 8
US-08-468-249A-3
; Sequence 3, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2051 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1846
US-08-468-249A-3

Query Match 22.2%; Score 445.2; DB 3; Length 2051;
Best Local Similarity 62.9%; Pred. No. 3.7e-133;
Matches 744; Conservative 0; Mismatches 423; Indels 15; Gaps 3;
QY 265 gaaaagtaattttccctgaatggatggactcatttttggccagaggaacatg 324
DB 383 GAGGCGTCCCTGTCGCCGAGTGGGACACATCGCTTGTGCGCCATATAGGGCCACG 442
QY 325 gaaaaatatcgctgttccatgcctcttatattatgacttcaaccataaaggattg 384
DB 443 GTGAAGTGGTGGCAGTACCTTGTCCCGATTACATTTATGACTTCAATCACAAAGGCCATG 502
QY 385 ctttccgaacttaaccccaatggaacatggaattttatgcacagcttaataaaacat 444
DB 503 CCTACAGACGCTGTGACCGAATGGCAGCTGGGAGTGTTCAGGGCACAACCGGACGT 562
QY 445 ggcccaattattcagactgccttcgtcttcgcagccagacatatacagataggaagaag 504
DB 563 GGCCCACTACAGGAGTGCGCTCAAGTTCATGACCAATGA-----GACCGGGGACGGG 616
QY 505 aattctgtgaacgctctatgtaagtataccgttggctactccatctcttttggttcc 564
DB 617 AGGTATTGACCGCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCTCCC 676
QY 565 tggctgtggtatctcattcattgttacttcagacgattgcatgactagaactata 624
DB 677 TCACGGTGGCTGTCTCATCTCGCTTATTTAGCGCGCTGCTCACTGCACGCAACTACA 736
QY 625 tccacatgaactatttgttcttcttcagctgagagctacaagcatcttctgtaaaagaca 684
DB 737 TCCACATGACATGTTCTCTCTGCTTTATGCTGCGCGCGGAGCATCTTCGTGAAGACG 796
QY 685 gagttagtccatgctcncatagaggaatgaaagagctggagctccctaaataatcagatgacc 744
DB 797 CTGTGCTTACTCTGGCTTTCACGCTGGATGAGGCCGAGCCCTCACAGAGAGAGTTCG 856
QY 745 cacaaaattccattgagggaactctctgtggacaaatc-----acaaatatcgtgggtgca 798
DB 857 ACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCGCGGTAGGCTACGCTGGCTGCC 916
QY 799 agattgctgtgtgattgtttatttacttctcgtgctacaataattatttgaatcctgtg 858
DB 917 GCGTGGCGGTGACCTTCTCTCTACTTCTCTGCTTCTGCTGCTACCAACTACTACTGGAATCTG 976

QY 859 aaggtctctacatgataaatactcatttggctgttcttttttgcgacacacaaacacctgt 918
DB 977 AGGGCTGTACTTGCACAGCCTCATCTTCATGGCGCTTTTTCAGAGAGAGAGTACCTGT 1036
QY 919 ggggtctcattttagataggtggggtttccagcagcaatttggcagcatgggctgtgg 978
DB 1037 GGGCTTTCACCATTTTGGCTGGGCTTACCGGCTCTCTCGTGGCTGTCTGGTGGTGGTG 1096
QY 979 cagagcaactctggtgctgaggtgctgggaacttagtgcggagacatcaagtgga 1038
DB 1097 TCAGAGCAACCTTGGCCAACTGGGTGCTGGGATCTGAGCTCCGGGCACAAAGAGTGA 1156
QY 1039 ttatcaagcaccgatcttagcagctattgggctgaattttattctgttttctgaatacgg 1098
DB 1157 TCATCCAGGTGCCCATCTCTGGCATCTGTGTGCTCAACTTCATCTTTTATCAACATCA 1216
QY 1099 ttagagtcttagctacaaaatctggagaccaaagtgagttgggcatgacacaggaagc 1158
DB 1217 TCCGGGTGCTTGGCACTAAGCTTCGGGAGACCAATGGCGCGCTGTGACACACGAGCAG 1276
QY 1159 aatacagaaactggccaaatcgacactggctcctggctccttagtcttggagtgcatata 1218
DB 1277 AGTACCGGAAGCTCTCAGGTCCACGTTGGTGTCTGCGCGCTCTTGGTGTCCACTACA 1336
QY 1219 tcgtgttctgtgctgcctcactcc---ttcactggggtcgtgggagagatccgcagtc 1275
DB 1337 CCGTCTTCATGGCTTGGCGTACACCGAGGTCTCAGGGACATTTGGCAGATCCAGATGC 1396
QY 1276 actgtgagctcttctcactcccttccagggttcttctgtgtctatcattctactgtact 1335
DB 1397 ATTATGAGATGCTTCAACTCCCTCCAGGATTTTGTGTGCCATCATATACTGTTTCT 1456
QY 1336 gcaatgagaggttcagcagagtgaaagatgtagagtcggtcggaatctctccgtgg 1395
DB 1457 GCAATGTGTGAGTGCAGCGAGAGATTAGGAAGTCATGAGCGCGCTGGACACTGCGGTGG 1516
QY 1396 actggaagaaagacaccgccatgtgcgcgcagatcgcgct 1437
DB 1517 ACTTCAAGCGCAAGCAGAGTGGAGTGGAGTACGACGTACAGCT 1558
RESULT 9
US-07-864-475A-4
Sequence 4, Application US/07864475A
Patent No. 5494806
GENERAL INFORMATION:
APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF INVENTION: AND DNA ENCODING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

Db 641 TGGGCTGTAAAGCAGCGCGTGGTGTATTCACAGTACTGTGTATGGCCAACTTCTTCTGGC 700
QY 850 tctgggtgaaggtctctacccgcataaactctcatctttgtggcttctcttttcggacacca 909
Db 701 TCGTGTGGAGGCGCTCTACTTGCACACCTACTTGCCTGTCTTCTCTGAGCGGA 760
QY 910 aatactgtggtggctctctctatagtaggctgggggtttccacagacatcttggcagcat 969
Db 761 AGTACTTCTGGGGGTACATATTCTGCTGGCTGGGGGTGCCAGCACCTTCATCATCTGTTCT 820
QY 970 gggctgtggcagcagcaactctgctgatgcagagtgcgtgggaacttagtgcgtggagaca 1029
Db 821 GGACCTCTCTCAGATTCATTTGAGGATATGGATGCTGGGACACCATCCACTCCTCTAC 880
QY 1030 tcaagtggatttataagcagcagctcttagcagctattggcgtgaattttattctgtttc 1089
Db 881 TGTGTGGATCATAAAGGCGCCCTCTCGCTCCATCTCTGTGTGAATTCATCTCTATTCA 940
QY 1090 tgaatcaggttagagttcttagtaccataaactctggagaccatgcagttgggcatgaca 1149
Db 941 TTTCGATCATCGAATCTTGTTCAGAACTGCGACCCCGACATGTCGGGAAGAGTGACA 1000
QY 1150 caaggaagcaatacaggaactggccaaactgacactggctcgtctcgtctgtttggag 1209
Db 1001 ACAG---CCATACTCGAGACTAGCCAGTCCACTCTTCTGTGATCCCTCTATTGGAG 1057
QY 1210 tgcattacatcgtgttcgtgctgcctcactcctcactggtcgtcgtgggtggagatcc 1269
Db 1058 TGCATCTACATCATGTTTGGCTTCTTCCCTTGACAAATTTAAGGCC-----GAAGTGA 1108
QY 1270 gcatgcactgtgagctctcttctcaactcctctcaggggtttcttctgtctatcactact 1329
Db 1109 AAATGCTCTTTCAGCTCATCGTGGGATCTTCCAGGGTGTGTGGTGCCATCTCTACT 1168
QY 1330 gctactgcaatgagaggttcaggcagaggtgaagaagatgtggagctgggtggaatc 1386
Db 1169 GCTTCTCAATGTTGAGGTGCGAGCGAGAGCTCGCGGGAAGTGGCGGCGCTGGCACC 1225

RESULT 12

US-08-811-897A-32
; Sequence 32, Application US/08811897A
; Patent No. 5858787
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSOYA, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABAYA, Yugo
; APPLICANT: SHIMAMOTO, No. 5858787io
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,897A
; FILING DATE: 05-MAR-1997

; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1401 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1401
US-08-811-897A-32

Query Match 5.9%; Score 118.8; DB 3; Length 1401;
Best Local Similarity 53.7%; Pred. No. 4.3e-28;
Matches 321; Conservative 0; Mismatches 262; Indels 15; Gaps 3;
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Db 728 TGTTCATTGGAAGCCCTGTACCTTTTACACTGCTGTTGGAGACCTTCTTCCCTGAGAGGA 787
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Db 788 GATATTTCTACTGTTACACCATCATCGGCTGGGGACACCTACTGTGTGTGTAACAGTGT 847
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Db 848 GGGCTGTGCTGAGGCTCTATTTTGTATGATGCGAGGATGCTGGGATATGAATGACAGCACAG 907
QY 1027 acatcaagtggatttatcaagcagcagctcttagcagctattggcgtgaattttattctct 1086
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QY 1087 ttctgaatcacggttagagttcttagctaccataaactctggagagaccaatgcagttgggcatg 1146
Db 968 TCATCGGCATCATCATCATCTTGTACAGAACTGCAGTCCCGCAGACATGGGAGGCAACG 1027
QY 1147 acacaaggaagcaatacaggaagaaactggccaaatcacactggtcctgtgctcctagttctg 1206
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QY 1327 actgtactgcaatggagaggttcaggcagaggtgaagaagatgtggagctcgtgggaa 1384
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RESULT 13

US-08-855-213-32
; Sequence 32, Application US/08855213
; Patent No. 5892004


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Db 1104 AGTCCAGCATCTACTTACGG---CTGGCCCGCTCCACCCCTACTGCTCTATCCCACTCTTCG 1160
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Db 1212 AAAGACTTGTGTTTGAAGCTTGGGCTGGGCTCCTTCCAGGGCTTTGTGGTGGCTGTACTCT 1271
Qy 1327 actactactgcaatggagaggttcagcacaggtgaaagagatgtgagtcggtggaa 1384
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Search completed: November 15, 2000, 20:32:48
Job time: 3920 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2000, 14:29:52 ; Search time 1010.91 Seconds
(without alignments)
12250.508 Million cell updates/sec

Title: US-09-236-468A-1
Perfect score: 2003
Sequence: 1 gttgctgtggcgagccaag.....atttgctgtgattgttca 2003

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*
12: gb_est12.*
13: gb_est13.*
14: gb_est14.*
15: gb_est15.*
16: gb_est16.*
17: gb_est17.*
18: gb_est18.*
19: gb_est19.*
20: gb_est20.*
21: gb_est21.*
22: gb_est22.*
23: gb_est23.*
24: gb_est24.*
25: gb_est25.*
26: gb_est26.*
27: gb_est27.*
28: gb_est28.*
29: gb_est29.*
30: gb_est30.*
31: gb_est31.*
32: gb_est32.*
33: gb_est33.*
34: gb_est34.*
35: gb_est35.*
36: gb_est36.*
37: gb_est37.*
38: gb_est38.*
39: gb_est39.*
40: gb_est40.*
41: em_estba.*
42: em_estfun.*
43: em_esthum1.*

44: em_esthum2.*
45: em_esthum3.*
46: em_esthum4.*
47: em_esthum5.*
48: em_esthum6.*
49: em_esthum7.*
50: em_esthum8.*
51: em_esthum9.*
52: em_esthum10.*
53: em_esthum11.*
54: em_esthum12.*
55: em_esthum13.*
56: em_esthum14.*
57: em_esthum15.*
58: em_esthum16.*
59: em_esthum17.*
60: em_esthum18.*
61: em_esthum19.*
62: em_esthum20.*
63: em_estin1.*
64: em_estin2.*
65: em_estin3.*
66: em_estin4.*
67: em_estom.*
68: em_estov1.*
69: em_estov2.*
70: em_estpl1.*
71: em_estpl2.*
72: em_estpl3.*
73: em_estpl4.*
74: em_estpl5.*
75: em_estrol.*
76: em_estro2.*
77: em_estro3.*
78: em_estro4.*
79: em_estro5.*
80: em_estro6.*
81: em_estro7.*
82: em_estro8.*
83: em_estro9.*
84: em_estro10.*
85: em_estro11.*
86: em_estro12.*
87: em_estro13.*
88: gb_gss1.*
89: gb_gss2.*
90: gb_gss3.*
91: gb_gss4.*
92: em_gss1.*
93: em_gss2.*
94: em_gss3.*
95: em_gss4.*
96: gb_gss5.*
97: gb_gss6.*
98: gb_gss7.*
99: gb_gss8.*
100: gb_gss9.*
101: em_gss5.*
102: em_gss6.*
103: em_gss7.*
104: em_gss8.*
105: em_gss9.*
106: em_gss10.*
107: em_gss11.*
108: gb_gss10.*
109: gb_gss11.*
110: em_gss12.*
111: gb_gss12.*
112: gb_gss13.*
113: gb_gss14.*
114: gb_gss15.*
115: gb_gss16.*
116: gb_gss17.*


```
Db 128 ACCTTGCCCAACACTGGGTGCTGGGACCTGAGCTCTGGGCACAAAGTGGATCATCCAG 187
      || |||| | | ||||| |||| | | |||| | | |||| | | |||| | | |||| | |
Qy 1047 gccgcatctagcagctattggctgaattttattctgttttctgaatacgggttagagtt 1106
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 188 GTGCCCATCTGCGCATCTGTGTGCTCAACTTCATCTCTTTATCAACATCATCCGGGTG 247
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1107 ctagctaccacaaatctggagacaaatcagttgggcatgacacaaaggaaagcaatacagg 1166
      || || || || || || || || || || || || || || || || || || || || ||
Db 248 CTTGCCCACTAAGCTTCCGGGAGACCAATGCGGGCGGTGTGCACACAGGAGCATACCGG 307
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1167 aaactggccaaaatcgacactggtcctgggtcttagtcttggagtgcaatcacatcgtgttc 1226
      || || || || || || || || || || || || || || || || || || || || ||
Db 308 AAGCTGCTCAGGTCCAGTGTGCTGTGTGCCACTCTTCGGGTGCCATACACCGCTTC 367
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1227 gttgctgcctcaactcct--tcactggctcgggtggagatccgcactgcactgtgagc 1284
      || || || || || || || || || || || || || || || || || || || || ||
Db 368 ATGGCCTTGGCTACACCGAGGTCTCAGGACACTGTGGCAGATCCAGATGCATATGAGA 427
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1285 tcttctcaactccttcagggtttcttggtctcatctactctactcactgcaatggag 1344
      || || || || || || || || || || || || || || || || || || || || ||
Db 428 TGCTCTCAACTCTCTCCAGGGATTTTGTTCCTCATATATACATCTTTTCTGCAATGGTG 487
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1345 aggttcaggcagggtgaagaagatggagtggtgggaatctctcgtggactggaaaa 1404
      || || || || || || || || || || || || || || || || || || || || ||
Db 488 AGGTGCAGGCAGAGATTAGGAAGTCTTGGAGCGCTGGACACTGGCATTTGGACTTCAAGC 547
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1405 ggcacgcgcattgtggcagccgcagatcgagct 1437
      || || || || || || || || || || || || || || || || || || || || ||
Db 548 GTAAAGCACGAAGGTGGAGTAGCAGCTACAGCT 580
      || || || || || || || || || || || || || || || || || || || || ||
```

RESULT 4

```
BE014986
LOCUS 126918 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence. 09-JUL-2000
DEFINITION BE014986
ACCESSION BE014986
VERSION BE014986.1 GI:8276022
KEYWORDS EST.
SOURCE Pig.
ORGANISM Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 542)
AUTHORS Fahrtenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
          Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
          and Keele,J.W.
          Design and use of two pooled tissue normalized cDNA libraries for
          EST discovery in swine
          Unpublished (2000)
          Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called and alt_trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 57 row: L column: 1
Seq primer: ATTAGCTGACACTATAG.
          Location/Qualifiers
            1..542
              /organism="Sus scrofa"
              /db_xref="taxon:9823"
              /clone_lib="MARC 1P1G"
              /tissue_type="pooled"
              /lab_host="DH10B"
              /note="Vector: pCMV SPORF6; Site_1: XbaI; Site_2: XhoI;
              Library made from pooled tissue from day 11, 13, 15, 20,
```

```
BASE COUNT 99 a 159 c 139 g 145 t
ORIGIN
Query Match 12.3%; Score 246.6; DB 32; Length 542;
Best Local Similarity 67.3%; Pred. No. 2.2e-61;
Matches 364; Conservative 0; Mismatches 174; Indels 3; Gaps 1;
Qy 800 gatttgctgttgatgtttatttaacttctcggctacaaattattattggtgatactggtgga 859
      || || || || || || || || || || || || || || || || || || || || ||
Db 2 GGTGTGCTGTGACCTTCTCTTACTTCTGCGCCACCAACTACTACTGATTCTTGGTGA 61
      || || || || || || || || || || || || || || || || || || || || ||
Qy 860 aggttctcactgcataatctcatcttctgtgcttcttcttcggacacacaaatcacctgtg 919
      || || || || || || || || || || || || || || || || || || || || ||
Db 62 GGGCTGTGACTGTCACAGCTCATCTTCATGCGCTTCCTCCGAGAAAGTAGTACCTGTG 121
      || || || || || || || || || || || || || || || || || || || || ||
Qy 920 gggcttcatttgataggctgggggtttccagcagcattgttgcagcatgggctgtggc 979
      || || || || || || || || || || || || || || || || || || || || ||
Db 122 GGGCTTTACAGTCTTCGGCTGGGTCTGCTGCATCTTCGTGGCTGCTGGGTCAAGTGT 181
      || || || || || || || || || || || || || || || || || || || || ||
Qy 980 acgagcaactcgtgctgatcgaggtgctgggaacttagtctggagacatcaagtggat 1039
      || || || || || || || || || || || || || || || || || || || || ||
Db 182 GAAAGCCACTCTGGCAACACCCGGGTGCTGGGACTTGAGCTCTGGGAACAGAAGTGGAT 241
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1040 ttatcaagcaccgatctcttagcagctattggctgaattttatttctgttctgaatacgt 1099
      || || || || || || || || || || || || || || || || || || || || ||
Db 242 CATCCAGTGGCCATCTGCGCTCCATTTGTGCTCAACTTCATCTTTCATCAACATTGT 301
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1100 tagagttctagctaccacaaatctgggagaccaaatgcagttgggcatgacacaaaggagca 1159
      || || || || || || || || || || || || || || || || || || || || ||
Db 302 CCGGCTCTTGCCACCAAGCTGCGGGAGACCAACGCCGCCGGTGTGACACGGCGCAGCA 361
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1160 atacaggaactggtgcaaatcgcacactggtcctggtcctagtttttggagtgcatcacat 1219
      || || || || || || || || || || || || || || || || || || || || ||
Db 362 GTACCGGAAGCTGCTCAAAATCCACACTGGTGTCTCATGCGCGCTCTTTGGGCTCCATTACAT 421
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1220 cgtgttcgtgctcctcactc---cttactcggctcgggtggagatccgcactgca 1276
      || || || || || || || || || || || || || || || || || || || || ||
Db 422 CGTCTTCATGGCTACGCCATACACTGAGGTCTCAGGAGCGCTTGGCAAGTCCAGATGCA 481
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1277 ctgtgagctcttcttcaactcctttcagggtttcttctgtctatcatctactgctactg 1336
      || || || || || || || || || || || || || || || || || || || || ||
Db 482 CTACGAGATGCTCTTCAACTCTCTCCAGGATTTTGTGTGTCATCATATACTGTGTTCTG 541
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1337 c 1337
Db 542 c 542
RESULT 5
AL043796
LOCUS 258 bp mRNA EST 29-FEB-2000
DEFINITION DKFZp434P0227_r1 434 (synonym: htes3) Homo sapiens cDNA clone
          DKFZp434P0227 5', mRNA sequence.
ACCESSION AL043796
VERSION AL043796.1 GI:5423180
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 258)
AUTHORS Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
          Wiemann,S.
          EST (Bloecker, et al.)
          Unpublished (1999)
          Contact: Bloecker H
          MIPS
          Am Klopferspitz 18a D-82152 Martinsried, Germany
          This is the 5' sequence of the clone insert
          Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
          Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
```

sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

s1 sequence also available.

This clone (DKFZp434P0227) is available at the R2PD in Berlin.

Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@r2pd.de.

FEATURES

source

```
1. .258
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434P0227"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
```

BASE COUNT 67 a 67 c 76 g 48 t

ORIGIN

```
Query Match 11.6%; Score 233; DB 14; Length 258;
Best Local Similarity 99.6%; Pred. No. 1.7e-57;
Matches 244; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1303 aggtttcttctgtctatctactgtctactgcaatgagaggttcaggcagagtgga 1362
|||||
DB 14 AGGTTCTTGTCTATCATCTACTACTGCTACTGCAATGGAGAGTTTCAGGCAGAGTGA 73
|||||
QY 1363 agaagatgtgagtcggtggaattctctcgttgactggaagaaagacacccgcatgtgca 1422
|||||
DB 74 AGAAGATGTGGAGTCGGTGAATCTCTCCGTGGACTCGAAAGGACACCGCCATGTGGCA 133
|||||
QY 1423 gccagatgcggctcagtgctcaccacgtgacgcacagcagcagcagtcacagg 1482
|||||
DB 134 CCCCAATGCGGCTCAGTCTCACCACCGTGACGCACAGCAGCAGCAGTCACAGG 193
|||||
QY 1483 tggcgg-cagcacacgcagtggtgtctatctctgtgcaagtgccaagatgcgcagcagcag 1541
|||||
DB 194 TGGCGGCAGCAGCACGCATGCTGTATCTCTGCGCAAGCTGCCAAGATGCCAGCAGAC 253
|||||
QY 1542 agcct 1546
|||||
DB 254 AGCCT 258
```

RESULT 6

```
LOCUS A0724325 369 bp DNA GSS 14-JUL-1999
DEFINITION HS_2107_AL_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2107 Col=11 Row=C, DNA sequence.
ACCESSION A0724325
VERSION A0724325.1 GI:5483994
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
```

```
REFERENCE 1 (bases 1 to 369)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
```

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>

Plate: 2107 row: C column: 11

Seq primer: M13 Reverse

Class: BAC ends

High quality sequence stop: 369.

FEATURES

source

```
1. .369
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2107 Col=11 Row=C"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
```

BASE COUNT 92 a 99 c 96 g 81 t 1 others

ORIGIN

```
Query Match 11.1%; Score 221.8; DB 108; Length 369;
Best Local Similarity 96.3%; Pred. No. 3.9e-54;
Matches 237; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
```

```
QY 1345 aggttcggcagagtggaagatgtggagtcgttggaatctctcgttgactggaaaa 1404
|||||
DB 124 ATGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGCTGGAACTCTCCGTGGACTGGA 183
|||||
QY 1405 ggaacccgcctatgagcagccagatgcgctcagtcagtcacccagcagcacagca 1464
|||||
DB 184 GGACACCCCATGTGGCAGCCGCGCAGATCGCGCTCAGTGCCTCACCACCGTGACGCACAGCA 243
|||||
QY 1465 ccagcagccagtcacagtggtgagg-cagcacacgcagtcgtgtctatctctgcaaaagctg 1523
|||||
DB 244 CCAGCAGCCAGTCACAAGTGGCGCCAGCACACATGTTGCTTATCTCTGGCANAGCTG 303
|||||
QY 1524 ccaagatgcgcagcagcagcctcagcagcacatcatttacctggtctatgtctggagta 1583
|||||
DB 304 CCAAGATGCGCAGCAGACAGCCTGACGCCACATCACTTTACCTGTCTATGCTGGAGTC 363
|||||
QY 1584 actcag 1589
|||||
DB 364 ACTCCG 369
```

RESULT 7

```
LOCUS AA240746 554 bp mRNA EST 12-MAR-1997
DEFINITION mv37all.r1 Guaywoodford Beier mouse kidney day 0 Mus musculus cDNA clone IMAGE:657212 5' similar to gb:X68596 PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE (HUMAN); gb:X78936 M.musculus mRNA for parathyroid hormone/parathyroid hormone (MOUSE ); mRNA sequence.
```

ACCESSION AA240746

VERSION AA240746.1 GI:1865137

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

```
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 554)
```

REFERENCE 1 (bases 1 to 554)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810


```

Qy 696 gctcacataggagtaaagagctggagtccttaataatgcaggatgacccacaaaattccc 755
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 TCTGGCTTCACGCTGGATGAGCCGAGCGCTCACGGAGGAGACTTCATATATCATCGCG 414
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 756 attgagggcaactcttgagacaatc-----acaatatatcggggtgcaagattgctgtg 810
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 415 CAGGTGCCGCTCGCCGCGCGCTGCTGGTACGCTGGCTGGCTGGCGCTGA 474
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 811 tgatgttattactctgctacaaattattattagatcctggtgaaagtctctacc 870
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 475 CTTCTCTCTACTCTGCTGCTACCACTACTACTGGAATCTGCTGGAGGAGCTGTA 534
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 871 tgcataatctcatcttctgtgcttcttcttcggacacacaaatctctggtggtctcatct 930
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 TACACAGCTCATCTTCATGCGCTTTTCTTAGAGAGAAGATATCTGTGGGGCTTCACAT 594
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 931 tgataggtcgtg 942
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 CTTTGGCTTGGG 606
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
BE294442 608 bp mRNA EST 20-JUL-2000
DEFINITION 601176049f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531181 5',
mRNA sequence.
ACCESSION BE294442
VERSION BE294442.1 GI:9177978
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 608)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM205 row: b column: 14
High quality sequence stop: 569.
Location/Qualifiers
1. .608
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3531181"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT
ORIGIN

Query Match 8.8%; Score 176.4; DB 34; Length 608;
Best Local Similarity 61.6%; Pred. No. 1.1e-40;
Matches 371; Conservative 0; Mismatches 166; Indels 65; Gaps 3;

```

Qy 792 ggggtgaagattgctgtgtgatgtttatttacttccctggctacaaaattatttggatc 851
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 50 GCCTGCAGGCTGGCTGTACACCTTCTCTTACTTCTGGCCACCACTACTACTGGATT 109
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 852 ctggtgaagagctctactcactgcataatctcttcttgggtcttcttcttgcacacaaa 911
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 110 CTGCTGGAGGGGCTGTACTCTGACAGGCTCATCTTCTATGGCTTCTTCTCAGAGAAGA 169
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 912 taccctggggctctcatcttgatagctgggggtttccacagcatttgttgcagcatgg 971
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 170 TACCTGTGGGCTTTCACAGTCTTCGGCTGG----- 199
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 972 gctgtggcagagcaactctgtgctgatcgagggtgctgggaacttagtgcgtggagacatc 1031
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 -----GGTGTGGGACTTCAGCTCCGGGAACAAA 228
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1032 aagtggattatcaagcacacgatcttagcagctatttgggtgaattttattctgttctg 1091
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 229 AAGTGGATCATCCAGGTGCCCATCTGGCCCTCCATTGTGCTCAACTTCATCTCTTCATC 288
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1092 aatacaggttagactctagctaccaaatactggagacacaaatcgagttggcgacacaca 1151
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 289 AATATGTCCTGGGTGCTGCGCCACCAAGCTGCGGAGACCAACGCCGCCGCTGTGACACA 348
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1152 aggaagcaatacaggaactggccaaatcgacacttgctcctggtccttagtcttcttggagt 1211
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 349 CGCGCAGCAGTACCGAAGCTGCTCAAAATCCACGCTGGTGTCTATGCCCTCTTTGGCGTC 408
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1212 cattacatcgtgtctgtgctgctcctcctcctcc-----ttcactgggctcgtgggagatc 1268
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 409 CACTACATTTGCTTCATGGCCACACCATACACCGAGGTCTCAGGGAGCGCTCTGGCAAGTC 468
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1269 cgeatgcactgtgagctctcttcaactccttccaggttcttcttcttctcat-catcta 1327
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 469 CAGATGCATATGAGATGCTCTTCACTCTCTCCAGGAGATTTTTCGCGCAATCCATATA 528
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1328 ctgctactgcaatggagaggttcaggcagagatgaaagaagtgtggagctcgtggaactc 1387
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 529 CTGTTTCTGCAACGGCGAGGTACAAGCTGAGATCCAGAAATCTTTGGAGCCCGCTGGAACA 588
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1388 ct 1389
|||
Db 589 CT 590

RESULT 10
AA034782 406 bp mRNA EST 23-AUG-1996
LOCUS mi52e07.r1 Soares mouse embryo NbMEI3.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:467172 5' similar to gb:X78936 M.musculus mRNA for
parathyroid hormone/parathyroid hormone (MOUSE);, mRNA sequence.
ACCESSION AA034782
VERSION AA034782.1 GI:1506554
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 406)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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QY 499 agcaagaattctgtgaacgocctctatgttaatgtatatacocttggctactccatctcttttg 558
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 16 AACGGAGGATTTTGACCGGCTGGGCATGATCTACACCGTGGGATATTCATGCTCTCTTG 75
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 559 gtccctggctgggtattcttcacatcttggttacttcaactgaagagattgcacttagga 618
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 76 CTTCCCTCACGGTGGCTGTGCTATCTAGCCTATTTTAGGGGCTGCACGTGCACGCGCA 135
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 619 actatcacacatgcattatttggctcttctcatgctgagagctacaagcatctttgtca 678
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 136 ACTACATCACATGCACATCTTCTCTGTTATGCTGGCGCGGAGACATCTTTCGTA 195
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 679 aagacagagtagtccatgctcacataggaagtaaaagagctggagtcctcctaataatgcag 738
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Db 196 AGGACGCTGTGCTTCTACTCTGCTTTCACGCTGGATCAGGCCGAGCGCTCACGGAGGAAG 255
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 739 atgaccacaaaattccattgaggaact-----tctgtggacaaaatcacaaatatatcg 792
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 256 AGTTGCATATCATCGCGCAGGTGCCGCTCCGCCCGCGCTGGCTACGCTG 315
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 793 ggtgcagattgctgtgtgagtgatttatttacttctcctggctcacaattatttggatcc 852
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 316 GCTGCCCTGTGGCGGTGACCTTCTCTCTACTTCTGTGCTACCACTACTACTGGATTC 375
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 853 tggtagaaggtctctacctgcataatctcatcttggcttcttcttcttgcggacacaaat 912
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 376 TGGTGGAGGACTGTACTTACACAGGCTCATCTTATGCGCTTTTCTCAGAGAAGAACT 435
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 913 acctgtggggcttcatctt 931
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 436 ATCTGTGGGGCTTCACCAT 454
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
AA240769 554 bp mRNA EST 12-MAR-1997
LOCUS mv37c11.r1 GuayWoodford Beier mouse kidney day 0 Mus musculus cDNA
DEFINITION clone IMAGE:657236 5' similar to gb:X68596 PARATHYROID
HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE (HUMAN); gb:X78936
M.musculus mRNA for parathyroid hormone/parathyroid hormone (MOUSE
);, mRNA sequence.
ACCESSION AA240769
VERSION AA240769.1 GI:1865143
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 554)
AUTHORS Marfa,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
THIS clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:403084
Seq primer: -28mi3 rev1 ET from Amersham
High quality sequence stop: 22.
Location/Qualifiers
1..554
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="IMAGE:657236"
/clone_lib="GuayWoodford Beier mouse kidney day 0"
/tissue_type="kidney"
/dev_stage="newborn (day 0)"
/lab_host="SOUR (kanamycin resistant)"
/note="organ: kidney; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; cloned unidirectionally. Primer:
Oligo df. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGGCAGGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3' Library provided
Lisa Guay-Woodford."
BASE COUNT 123 a 147 c 143 g 141 t
ORIGIN
Query Match 7.4%; Score 148.2; DB 2; Length 554;
Best Local Similarity 66.4%; Pred. No. 2.1e-32;
Matches 273; Conservative 0; Mismatches 133; Indels 5; Gaps 4;
QY 1032 aagtggtattatcaagcaccgactcttagcagctattggctgaattttattctgtttctg 1091
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 AAGTGGATCATCCAGGTGCCCATCTCGGCTGCTGTGCTCAACTTCATCTCTTTATG 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1092 aatacgggttagagttcttagctaccacaaatctgggagaccaatgc-agttgggcatgacac 1150
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 AACATCATCCGGGTGCTTGGCCTTAAGCTTCGTGAGACCAATCGCGCGCTGTGTGACAC 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1151 aaggagcaatacacagaaaactggccaaatcgacactggtcctggtccttagtctt-tggag 1209
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 122 CAGGACAGTAGTACCGGAAGCTGCTCATGTCCACGTTGGTGCCTGTGCCACTCTTCGGGTG 181
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1210 tgcattacatcgtgttcgtgctgcctgcct--cactccttcactgggctcggtggagagat 1267
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 182 TCCACTACACCGTCTTCATGCGCTTCGCTACACCGAGGTCTCAGGACACTGTGGCAGAT 241
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1268 cgcgtgactgagctcttcttcaactccttcagggt-tttctttgtgtctatcatc 1326
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 242 CCAGATGCATCATGAGATGCTCTCAACTCCTTCAGGAGATTTTGGTGGCATCATAT 301
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1327 actgctactgcaatgagagaggttcaggcagagagtggaagaagatgtggagtcggtggaatc 1386
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 302 ACTGTTTCTGCAATGGTGAGGTTTCATGTCAGAGATTAAAGAAAGTCTTGGAGCGCTTGACAC 361
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1387 tctccgtggaactggaaaaggacacccgcaatgtgagccgagatgcggct 1437
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 362 TGGCATTGGACTTCAAGCGTAAAGCAGCAAGTTGAAGTAGCAGCTAAAGCT 412
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 15
AA987157/c 827 bp mRNA EST 28-MAY-1998
LOCUS uc81a02.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
DEFINITION IMAGE:1432010 3' similar to gb:X78936 M.musculus mRNA for
parathyroid hormone/parathyroid hormone (MOUSE);, mRNA sequence.
ACCESSION AA987157
VERSION AA987157.1 GI:3167920
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 827)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Search completed: November 15, 2000, 19:45:57
Job time: 18965 sec

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